

GenCore version 5.1.3

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OM Protein - protein search, using sw model

Run on:

December 12, 2002, 15:09:28 | Search time 32.4 Seconds
(without alignments)
24.676 Million cell updates/sec

Title: US-09-600-432-24

Sequences: 3

Sequences: 3

Sequences: 3

Scoring table: BLOSUM62

Gap: 10.0, Gapext: 0.5

Searched: 904470 seqs, 13325020 residues

Total number of hits satisfying chosen parameters: 42205

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

A: Genesep_101002.*

1: /SID52/gcdata/genesep/emb1/AA1980.DAT.*
 2: /SID52/gcdata/genesep/emb1/AA1981.DAT.*
 3: /SID52/gcdata/genesep/emb1/AA1982.DAT.*
 4: /SID52/gcdata/genesep/emb1/AA1983.DAT.*
 5: /SID52/gcdata/genesep/emb1/AA1984.DAT.*
 6: /SID52/gcdata/genesep/emb1/AA1985.DAT.*
 7: /SID52/gcdata/genesep/emb1/AA1986.DAT.*
 8: /SID52/gcdata/genesep/emb1/AA1987.DAT.*
 9: /SID52/gcdata/genesep/emb1/AA1988.DAT.*
 10: /SID52/gcdata/genesep/emb1/AA1989.DAT.*
 11: /SID52/gcdata/genesep/emb1/AA1990.DAT.*
 12: /SID52/gcdata/genesep/emb1/AA1991.DAT.*
 13: /SID52/gcdata/genesep/emb1/AA1992.DAT.*
 14: /SID52/gcdata/genesep/emb1/AA1993.DAT.*
 15: /SID52/gcdata/genesep/emb1/AA1994.DAT.*
 16: /SID52/gcdata/genesep/emb1/AA1995.DAT.*
 17: /SID52/gcdata/genesep/emb1/AA1996.DAT.*
 18: /SID52/gcdata/genesep/emb1/AA1997.DAT.*
 19: /SID52/gcdata/genesep/emb1/AA1998.DAT.*
 20: /SID52/gcdata/genesep/emb1/AA1999.DAT.*
 21: /SID52/gcdata/genesep/emb1/AA2000.DAT.*
 22: /SID52/gcdata/genesep/emb1/AA2001.DAT.*
 23: /SID52/gcdata/genesep/emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SDMMATES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	2	32	100.0	6	21	AA19851	Beta-1 integrin
2	3	25	78.1	5	18	AA19855	Amino acid sequence
3	25	78.1	5	18	AA19842	Chimeric integrin co	
4	25	78.1	5	20	AA19852	Beta-1 integrin co	
5	25	78.1	5	20	AA19851	Beta-1 integrin co	
6	25	78.1	5	21	AA19066	Amino acid sequence	
7	25	78.1	5	21	AA19067	Amino acid sequence	
8	25	78.1	5	21	AA19068	Amino acid sequence	
9	20	62.5	4	21	AA19058	Beta-1 integrin co	
10	19	59.4	6	20	AA125842	Human secreted pro	

11	18	56.2	5	19	AA23060	Human p53 cellular
12	18	56.2	5	19	AA23060	Analogous of chym
13	18	56.2	5	22	AA11144	Chymotrypsin pepti
14	17	53.1	5	22	AA11144	Transposon peptid
15	17	53.1	5	6	AA20198	Analogous of chym
16	17	53.1	5	19	AA17462	Human saliva psp-1
17	17	53.1	5	22	AA19762	Human saliva psp-1
18	17	53.1	5	22	AA19762	Human saliva psp-1
19	17	53.1	5	22	AA19762	Human saliva psp-1
20	17	53.1	5	22	AA19762	Human saliva psp-1
21	17	53.1	5	22	AA19762	Human saliva psp-1
22	17	53.1	5	22	AA19762	Human saliva psp-1
23	17	53.1	5	22	AA19762	Human saliva psp-1
24	17	53.1	5	22	AA19762	Human saliva psp-1
25	17	53.1	5	22	AA19762	Human saliva psp-1
26	17	53.1	5	22	AA19762	Human saliva psp-1
27	17	53.1	5	22	AA19762	Human saliva psp-1
28	17	53.1	5	22	AA19762	Human saliva psp-1
29	17	53.1	5	22	AA19762	Human saliva psp-1
30	17	53.1	5	22	AA19762	Human saliva psp-1
31	17	53.1	5	22	AA19762	Human saliva psp-1
32	17	53.1	5	22	AA19762	Human saliva psp-1
33	17	53.1	5	22	AA19762	Human saliva psp-1
34	17	53.1	5	22	AA19762	Human saliva psp-1
35	17	53.1	5	22	AA19762	Human saliva psp-1
36	17	53.1	5	22	AA19762	Human saliva psp-1
37	17	53.1	5	22	AA19762	Human saliva psp-1
38	16	50.0	4	10	AA19520	Recombinant MSV ge
39	16	50.0	4	10	AA19520	Recombinant MSV ge
40	16	50.0	4	19	AA19578	Transmembrane pepti
41	16	50.0	4	19	AA19578	Transmembrane pepti
42	16	50.0	4	20	AA14261	Human 198 peptide
43	16	50.0	4	20	AA14261	Human 198 peptide
44	16	50.0	4	23	AA17908	Thrombin inhibitor
45	16	50.0	5	7	AA10016	Sequence of frame
						Human growth norma

ALIGNMENTS

RESULT 1
 AA23511
 ID AA23511 standard; peptide: 6 AA.
 XX AA23511
 XX AA23511

DT 19-OCT-1999 (first entry)
 DE Beta-1 Integrin cell adhesion modulator analogue #24.

XX Beta-1 integrin dependent cell adhesion; LIGAND motif: tumour;
 XX C-terminal cysteine tagged, cancer; fibronectin, melanoma.
 XX Synthetic.
 OS Synthetic.
 PH MO997669-AL.
 XX 29-JUL-1999.
 XX 21-JAN-1999: 99MO-080126.
 XX 12-NOV-1998: 98US-0096212.
 XX 12-JAN-1998: 98US-0072119.
 XX 12-NOV-1998: 98US-0096211.
 XX (MIND) UNIV MINNESOTA.
 XX Briscoe A, Furcht LT, McCarthy JB;
 XX WPI: 1999-46912/39.
 XX New peptides modulating beta1 integrin subunit dependent cell
 XX adhesion, useful to study cell adhesion e.g. epithelial integrin

Query Match 78.1%; Score 25; DB 18; Length 5;
 .Best Local Similarity 100.0%; Pred. No. 7.8e05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRR1 5
 DB 1 PRR1 5

RESULT 4
 AA178512
 AC AA178512 standard; peptide; 5 AA.
 ID AA178512
 DE 19-OCT-1999 (first entry)
 XX Beta-1 integrin cell adhesion modulator analogue #25.
 XX Beta-1 integrin dependent cell adhesion; LIPAR motif; tumour;
 XX C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX Synthetic.
 XX W0937669-AL.
 XX 29-JUL-1999.
 XX 21-JAN-1999; 99MO-0801236.
 XX 12-AUG-1998; 98US-0096212.
 XX 12-AUG-1998; 98US-0072119.
 XX 12-AUG-1998; 98US-0096211.
 XX (MIMU) UNIV MINNESOTA.
 XX Brienza A, Furcht LT, McCarthy JB;
 XX WPI; 1999-469112/39.
 XX New peptides modulating beta1 integrin subunit dependent cell
 XX adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin
 XX dependent adhesion important in tumour cell biology
 XX Claim 6; Fig 7; 47pp; English.

This sequence is a C-terminal tyrosine tagged peptide. This peptide
 inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 which modulate beta-1 integrin subunit dependent cell adhesion used a
 C-terminal amino acid residue (AR) which has a side chain including an
 aromatic group, a penultimate C-terminal amino acid residue (LIP) with
 an alkyl side chain, and a penultimate C-terminal amino acid residue
 (LIP) with an alkyl side chain. These peptides have also shown that
 inhibiting peptides do not contain D-amino acids and that it is the
 presence of the Artp motif that conveys effective beta1 integrin
 inhibition. The beta-1 integrin subunit dependent cell adhesion is
 important for cell adhesion to extracellular matrix proteins, and the
 presence of these peptides expressed on tumours such as melanomas.
 treatment of cancer.

Query Match 78.1%; Score 25; DB 20; Length 5;
 .Best Local Similarity 100.0%; Pred. No. 7.8e05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRR1 6
 DB 1 PRR1 5

RESULT 6
 AA19066
 AC AA19066 standard; peptide; 5 AA.
 ID AA19066
 DE 08-FEB-2001 (first entry)
 XX Amino acid sequence of a beta1-integrin inhibitor.
 XX Beta1-integrin inhibitor; leukocyte mediated tissue destruction;
 XX central nervous system ischemic injury, myocardial infarction.

RESULT 5
 AA178546
 AC AA178546 standard; peptide; 5 AA.
 ID AA178546
 DE 19-OCT-1999 (first entry)
 XX Beta-1 integrin cell adhesion modulator analogue #39.
 XX Beta-1 integrin dependent cell adhesion; LIPAR motif; tumour;
 XX C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX Synthetic.
 XX W0937669-AL.
 XX 29-JUL-1999.
 XX 21-JAN-1999; 99MO-0801236.
 XX 12-AUG-1998; 98US-0096212.
 XX 12-JAN-1998; 98US-0072119.
 XX 12-AUG-1998; 98US-0096211.
 XX (MIMU) UNIV MINNESOTA.
 XX Brienza A, Furcht LT, McCarthy JB;
 XX WPI; 1999-469112/39.
 XX New peptides modulating beta1 integrin subunit dependent cell
 XX adhesion, useful to study cell adhesion e.g. alpha4beta1 integrin
 XX dependent adhesion important in tumour cell biology
 XX Example 11; Fig 15; 47pp; English.

This peptide is used with AA178510-178516 to show that peptides
 which modulate beta-1 integrin subunit dependent cell adhesion used a
 C-terminal amino acid residue (AR) which has a side chain including an
 aromatic group, a penultimate C-terminal amino acid residue (LIP) with
 an alkyl side chain, and a penultimate C-terminal amino acid residue
 (LIP) with an alkyl side chain. These peptides have also shown that
 inhibiting peptides do not contain D-amino acids and that it is the
 presence of the Artp motif that conveys effective beta1 integrin
 inhibition. The beta-1 integrin subunit dependent cell adhesion is
 important for cell adhesion to extracellular matrix proteins, and the
 presence of these peptides expressed on tumours such as melanomas.
 treatment of cancer.

Query Match 78.1%; Score 25; DB 20; Length 5;
 .Best Local Similarity 100.0%; Pred. No. 7.8e05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRR1 5
 DB 1 PRR1 5

RESULT 6
 AA19066
 AC AA19066 standard; peptide; 5 AA.
 ID AA19066
 DE 08-FEB-2001 (first entry)
 XX Amino acid sequence of a beta1-integrin inhibitor.
 XX Beta1-integrin inhibitor; leukocyte mediated tissue destruction;
 XX central nervous system ischemic injury, myocardial infarction.

kw beta1-integrin; angioplasty, surgical incision; injury-related trauma;
 CC transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 CC Synthetic.

XX W0200056350-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000MO-US07640.

XX 22-MAR-1999; 9905-0125634.

XX 24-NOV-1999; 9905-017538.

XX (MIMU) UNIV MINNESOTA.

XX (TEMA) UNIV TEXAS SYSTEM.

XX (SEMT-) SEMTROM MEDICAL INC.

XX McCarthy JB, Milecki WJ, Jamieson GA, Low WC, Sawchuk RJ;

XX Furcht LF;

XX WPI: 2000-65062/63.

XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
 CC a patient, comprises administering a peptide inhibitor of
 CC beta1-integrin, useful for treatment of e.g. cancer and osteoporosis -

XX Claim 3; Page 38; 61pp; English.

XX AAB19051-67 represent beta1-integrin inhibitors. The peptides inhibit

CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC angioplasty, surgical incisions, injury-related trauma, and/or

CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.

XX Sequence 5 AA;

XX Query Match

XX Best Local Similarity 78.18; Score 25; DB 21; Length 5;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRAR1 5

Db 1 PRAR1 5

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PR 22-MAR-1999; 9905-0125634.

PR 24-NOV-1999; 9905-017538.

XX (MIMU) UNIV MINNESOTA.

XX (TEMA) UNIV TEXAS SYSTEM.

XX (SEMT-) SEMTROM MEDICAL INC.

XX McCarthy JB, Milecki WJ, Jamieson GA, Low WC, Sawchuk RJ;

XX Furcht LF;

XX WPI: 2000-65062/63.

XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
 CC a patient, comprises administering a peptide inhibitor of
 CC beta1-integrin, useful for treatment of e.g. cancer and osteoporosis -

XX Claim 3; Page 38; 61pp; English.

XX AAB19051-67 represent beta1-integrin inhibitors. The peptides inhibit

CC destruction. The peptides are useful for inhibiting inflammatory
 CC leukocyte mediated destruction of tissue which occurs as a result of
 CC angioplasty, surgical incisions, injury-related trauma, and/or

CC transplant reperfusion, exposure to heat, cold, light, electricity
 CC and/or chemicals. They are also useful for the treatment of stroke, a
 CC burn type injury, cancer, and osteoporosis.

XX Sequence 5 AA;

XX Query Match

XX Best Local Similarity 78.18; Score 25; DB 21; Length 5;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PRAR1 6

Db 1 PRAR1 5

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XX Claim 6; Fig 9; 47pp; English.

XX This sequence is a C-terminal tyrosine tagged peptide. This peptide
 XX inhibits beta-1 integrin subunit dependent cell adhesion. Peptides
 XX AA04510-04515 have been used to show that peptides which modulate this
 XX interaction are useful for the treatment of cancer. The peptide which
 XX has a side chain including an aromatic group, and a penultimate
 XX C-terminal amino acid residue (Lip) with an alkyl side chain group. i.e.
 XX inhibiting peptides do not contain D-amino acids and that L in the
 XX presence of the AALip motif that conveys effective beta1 integrin
 XX inhibition is important for cell adhesion. The beta1 integrin subunit dependent
 XX cell adhesion is important for cell and tumor growth. The beta1
 XX proteins, and the subunit is expressed on tumours such as melanoma.
 XX Therefore these Liptr motif containing peptides may be important in the
 XX treatment of cancer.

XX Sequence 4 AA:
 XX Query Match 52.5%; Score 20; DB 20; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 7, de:05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 3 AMY 6
 XX I I I I
 XX DQ 1 AMY 4

XX Result 9
 XX ID AAB19068 standard; peptide; 4 AA.
 XX XX AAB19068;
 XX 09-FEB-2001 (first entry)

XX Amino acid sequence of a beta1-integrin inhibitor.
 XX XX
 XX Beta1-integrin inhibitor; leukocyte mediated tissue destruction;
 XX beta1-integrin; angioplasty; surgical incision; injury-related trauma;
 XX transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX Synthetic.

XX W2000056350-A2.
 XX 28-SEP-2000.
 XX 22-MAR-2000; 2000WO-0507680.
 XX 22-MAR-1999; 98US-0125634.
 XX 24-NOV-1999; 99US-0167538.
 XX (MING) UNIV MINNESOTA.
 XX (TEXA) UNIV TEXAS SYSTEM
 XX (GENT) STRAHLER MEDICAL INC.
 XX McCarthy TG, Milecki WJ, Jamieson GA, Low WC. Sawchuk RJ;
 XX Furcht LT;
 XX WPI; 2000-65062/53.
 XX Inhibition of inflammatory leukocyte mediated destruction of tissue in
 XX a patient, comprising administering a peptide inhibitor of
 XX beta1-integrin, useful for treatment of e.g. cancer and osteoporosis
 XX Claim 3; Page 38; 6pp; English.

XX AAB19064, 67 represent beta1-integrin inhibitors. The peptides inhibit
 XX beta1-integrin subunit dependent cell adhesion and tumor growth
 XX destruction. The peptides are useful for inhibiting inflammatory

XX leukocyte mediated destruction of tissue which occurs as a result of
 XX central nervous system (CNS) ischemic injury, myocardial infarction,
 XX angioplasty, surgical incisions, injury-related trauma, and/or
 XX chemotherapy. The peptides are useful for preventing, treating or
 XX and/or chemicals. They are also useful for the treatment of stroke, a
 XX burn type injury, cancer, and osteoporosis.

XX Sequence 4 AA:
 XX Query Match 52.5%; Score 20; DB 21; Length 4;
 XX Best Local Similarity 100.0%; Pred. No. 7, de:05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 3 AMY 6
 XX I I I I
 XX DQ 1 AMY 4

XX Result 10
 XX ID AYZ25844 standard; protein; 6 AA.
 XX XX AYZ25844;
 XX 04-OCT-1999 (first entry)

XX Human secreted protein fragment encoded from gene 49.
 XX XX
 XX Secreted protein; human; treatment; diagnosis; therapy; cancer; tumor;
 XX neurodegenerative disorder; developmental abnormality; blood disorder;
 XX autoimmune disease; hepatitis; leukemia; immune system; inflammation;
 XX ischemic shock; Alzheimer's disease; cognitive disorder; schizophrenia;
 XX cardiovascular disorder; wound healing; stroke; arthritis; obesity;
 XX diabetes; postnatal; transplant rejection; infection; AIDS;
 XX metabolic disorder.
 XX Homo sapiens.
 XX W09938881-AL.
 XX 05-AUG-1999.

XX 99MO-0801621.
 XX 30-JAN-1998; 98US-0073170.
 XX 30-JAN-1998; 98US-0073159.
 XX 30-JAN-1998; 98US-0073159.
 XX 30-JAN-1998; 98US-0073160.
 XX 30-JAN-1998; 98US-0073161.
 XX 30-JAN-1998; 98US-0073162.
 XX 30-JAN-1998; 98US-0073164.
 XX 30-JAN-1998; 98US-0073165.
 XX 30-JAN-1998; 98US-0073167.
 XX (HUMA) HUMAN GENEOME SCI INC.
 XX Carter RC, Endress GA, Peng P, Ferrie AM, Florence C;
 XX Florence KA, Jant F, M J, Rosen CA, Rubin SM;
 XX Forrester CH, Young P, Yu G;
 XX WPI; 1999-469315/39.
 XX X-7508; A200436.
 XX New isolated human genes and the secreted polypeptides they encode
 XX useful in, e.g. treatment of Alzheimer's
 XX Disclosures: Page 365; 39pp; English.

XX This invention describes novel human genes (see AA00410-00477) and the
 XX secreted proteins (see AYZ25711-Y25778) and fragments (see
 XX AA25779-Y25907) they encode. The polynucleotides and their corresponding
 XX secreted polypeptides are useful for preventing, treating or ameliorating
 XX medical conditions e.g. by protein or gene therapy. Also pharmacol

CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC polynucleotides of the invention. based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis
 CC of various diseases, including but not limited to: autoimmune diseases,
 CC developmental abnormalities and fetal deficiencies, blood disorders,
 CC leukemias, diseases of the immune system, autoimmune diseases, hepatic
 CC and renal disease, inflammation, allergies, ischemic shock, Alzheimer's
 CC disease, diabetes, multiple sclerosis, rheumatoid arthritis, asthma, sepsis,
 CC disorders, wound healing, stroke, arthritis, obesity, asthma, sepsis,
 CC acne, psoriasis, transplant rejection, metabolic disorders, infections
 CC and cancer. The polypeptides are also useful for identifying their binding
 CC partners.

XX Sequence 6 AA:

Query Match 56.4% Score 19; DB 20; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARVY 6

DB 1 ARVY 4

RESULTS 11
 ID ANY21160
 AC ANY21060

Human p53 cellular tumour antigen mutant protein fragment 7.

XX 22-JUL-1999 (first entry)

XX Human beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 XX Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 XX diabetes mellitus type II; microtubule associated protein; Big Tau;
 XX ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 XX neurofilament-F; presenilin 1; presenilin 2; cellular tumour antigen;
 XX bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; BMSF-C; NP-A;
 XX high mobility group protein-C; neuroendocrine specific protein A.

XX Homo sapiens.

XX W09843322-32.

XX 15-OCT-1998.

XX 02-APR-1998.

XX 10-APR-1997.

XX (UYUT.) RIKESUNIV UTRECHT.

XX (ROYA.) ROYAL METERIUMS ACID ARTS & SCI.

XX (UYUT.) UNIV AUTISMUM ERMINGHAM.

XX Burbach JPH, Grosveld PG, Van Leeuwen FM;
 XX N-PS2B; AAT7365.

XX WPI: 1998-60990/41.

XX Diagnosing diseases by detecting frameshift mutations in RNA or
 XX corresponding protein mutations - used to diagnose cancer and also
 XX neurological diseases, particularly Alzheimer's disease, and also
 XX treatment and prevention with specific ribozymes or wild-type
 XX RNA

Disclosure: Figure 14; 25pp; English.

XX This invention describes a novel method for the diagnosis of a disease
 CC mutation, by or associated with, an RNA molecule that has a frameshift
 CC disease and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Huntington's disease, Parkinson's disease, multiple sclerosis,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC is based on the observation that the disease may be caused by mutations
 CC in an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC beta-amyloid precursor protein, the amyloid precursor protein, including
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M, acidic
 CC protein (GAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, xenobiotic II, HSPF-1, high mobility group
 CC protein-C (HMGPC) and neuroendocrine specific protein A.

XX Sequence 5 AA:

Query Match 56.2% Score 18; DB 19; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRA 4

DB 2 PRA 5

RESULTS 12

ID ANY74620

AC ANY74620

Analogue of chymotrypsin-cleaved

XX 21-DEC-1998 (first entry)

XX Analogue of chymotrypsin-cleaved

XX Human; urokinase receptor; UPAR; soluble UPAR; SUPAR; chymotrypsin;
 XX wound healing; antigen vaccination; HIV.

XX Homo sapiens.

XX W09842733-AL.

XX 01-OCT-1998.

XX 18-MAR-1998.

XX 20-MAR-1997.

XX (GUT.) UNIV ALIUM STUD.

XX (GARR.) ROMO CENT SAN RAFAELE DEL MONTE TABOR.

XX Blasi F, Pazioli F, Nicolai S, Resnati M;
 XX WPI: 1998-531945/45.

XX New soluble urokinase receptor products obtained by chymotrypsin
 XX cleavage, for the treatment of thrombotic diseases
 XX and inflammatory disorders or for stimulating wound healing

XX Disclosure: Page 13; 5pp; English.

XX This is the nucleotide sequence of a functional analogue of the
 XX chymotrypsin-cleaved urokinase receptor (UPAR) protein, which
 XX perturbed in the method of the invention. This protein
 XX products obtained by chymotrypsin cleavage is used to treat cancer.

Job Time : 33.4 secs

CC membrane of lung cells.

XX Sequence 5 AA;

SQ Query Match

XX Best Local Similarity 56.2%; Score 18; DB 23; Length 5;

XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRAR 4

DB 1 PRAR 4

RESULT 15

AMPS0198

XD MAP50198 standard; peptide; 5 AA.

XX AC MAP50198;

XX AC MAP50198;

XX 17-OCT-1991 (first entry)

DE Sequence of oligopeptide 1 specific to the beta-subunit of human

XX chorionic gonadotropin (hCG).

KW Contraception; assay; pregnancy test; luteinising hormone;

XX human chorionic gonadotropin.

XX OS Homo sapiens.

XX XX EPI42387-A.

XX PD 22-MAY-1985.

XX 23-JUN-1984; 84EP-0401710.

XX PR 25-AUG-1983; 83EP-0401714.

XX 23-AUG-1984; 84EP-0401710.

XX PA (ANDA-) ANDA BIOLOGICALS.

XX PT Meas RF;

XX WPI; 1985-124152/21.

XX Prepn. of anti-hCG and anti-LH vaccines - by use of

XX oligo-peptide(s) specific to beta-sub-unit of LH and hCG

XX Claim 1; Page 17; 22pp; English.

XX CC Oligopeptides MAP50198-950705, specific to the beta-subunit of LH and

XX of hCG coated near of anti-hCG and anti-LH vaccines. The vaccines

XX are characterised in that these oligopeptides are complexed upon

XX own beta-subunit of hCG and LH or upon oligopeptides containing

XX cysteine whose AA chain is common to LH and hCG, namely the peptides

XX are administered by injection in vaccinees. The specific oligopeptides

XX antibodies so that a contraceptive effect is achieved; and the

XX antibodies are also useful in assays for hCG and LH in body fluids.

SQ Query Match

XX Best Local Similarity 53.1%; Score 17; DB 6; Length 5;

XX Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4

DB 1 PRAR 4

Search completed: December 12, 2002, 15:17:15


```

1 APPLICANT: Allen, Jenise B.
2 APPLICANT: Billups, Kevin L.
3 APPLICANT: Everett, Jeffrey E.
4 APPLICANT: Finkbeiner, David A.
5 TITLE OF INVENTION: Treating Inflammatory
6 DISEASES USING POLYPEPTIDES WITH FIBRONECTIN ACTIVITY
7 NUMBER OF SEQUENCES: 15
8 CORRESPONDENCE ADDRESS:
9 STREET: 90 South 7th Street, 3100 No. 5840691west Center
10 CITY: Minneapolis
11 STATE: Minnesota
12 COUNTRY: USA
13 ZIP: 55402
14 CONTACT PERSON: NAME:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/480.133A
20 PRIORITY NUMBER: 08/139.903
21 CLASSIFICATION: 514
22 PILLING DATE: 21-OCT-1993
23 PRIOR APPLICATION DATA: US 08/139.903
24 APPLICATION NUMBER: US 07/990.296
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Carter, Charles G.
27 TELEPHONE: 612-332-9031
28 TELECOMMUNICATION INFORMATION:
29 REFERENCE/DOCKET NUMBER: 600-308US01
30 INFORMATION FOR SEQ ID NO: 13:
31 SEQUENCE CHARACTERISTICS:
32 TYPE: amino acid
33 STRANDNESS:
34 MOLECULE TYPE: Peptide
35 FRAGMENT TYPE: Internal
36 US-08-480-133A-15 linear
37
38 Query Match 56.2% Score 18; DB 2; Length 4;
39 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
40 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
41
42 QY 2 PART 5
43 DB 1 PART 4
44
45 RESULT 3
46 US-09-008-30-30
47 Sequence 13 Application US/09/008308
48 Patent No. 6080575
49 GENERAL INFORMATION:
50 APPLICANT: Mueller, Hans H.
51 APPLICANT: Mueller, Rolf
52 APPLICANT: Sack, Hans-Harald
53 TITLE OF INVENTION: CONSTRUCT FOR EXPRESSING
54 ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
55 PREPARATION AND USE
56 NUMBER OF SEQUENCES: 62
57 CORRESPONDENCE ADDRESS:
58 STREET: 3000 K Street, N.W., Suite 500
59 CITY: Washington
60 STATE: D.C.
61 COUNTRY: USA
62 MEDIUM TYPE: Floppy disk

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1 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/008.308
5 PILLING DATE: 16-JAN-1998
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: DE 397 01 141.1
8 PRIORITY NUMBER: 397 01 141.1
9 ATTORNEY/AGENT INFORMATION:
10 NAME: Sandercock, Colin G.
11 REGISTRATION NUMBER: 11.285
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (202)672-5300
14 TELEFAX: (202)672-5395
15 TELEX: 941136
16 INFORMATION FOR SEQ ID NO: 30:
17 SEQUENCE CHARACTERISTICS:
18 TYPE: amino acid
19 STRANDNESS:
20 MOLECULE TYPE: Peptide
21 FRAGMENT TYPE: Internal
22 US-09-008-308-30
23
24 Query Match 56.2% Score 18; DB 3; Length 4;
25 Best Local Similarity 100.0%; Pred. No. 1.9e-05;
26 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
27
28 QY 2 PART 5
29 DB 1 PART 4
30
31 RESULT 4
32 US-09-381-2448-13
33 Sequence 13 Application US/09/3812448
34 Patent No. 6465710
35 GENERAL INFORMATION:
36 APPLICANT: BLASI, Francesco
37 APPLICANT: BRESNAHAN, James
38 APPLICANT: RESNATI, Massimo
39 APPLICANT: NICOLAI, Sidenius
40 TITLE OF INVENTION: Immunomodulating Peptide
41 FILE REFERENCE: 0471-0143P
42 CURRENT APPLICATION NUMBER: US/09/381.2448
43 CURRENT PILLING DATE: 2000-10-20
44 PRIOR FILING DATE: 1998-03-18
45 PRIOR FILING DATE: 1998-03-18
46 NUMBER OF SEQ ID NOS: 28
47 SEQ ID NO 13
48 SEQ ID NO 13
49 LENGTH: 5
50 STRANDNESS:
51 ORGANISM: Artificial Sequence
52 OTHER INFORMATION: Description of Artificial Sequence: synthetic
53 peptide analogue of the human UPRN
54 US-09-381-2448-13
55
56 Query Match 56.2% Score 18; DB 4; Length 5;
57 Best Local Similarity 75.0%; Pred. No. 1.9e-05;
58 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
59
60 QY 1 PART 4
61 DB 1 PART 4
62
63 RESULT 5

```



```

Query Match      53.1k; Score 17; DB 3; Length 6;
Best Local Similarity 75.0k; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 RARI 5
Db      2 RARI 5

US-09-326-440-57
RESULT 11
US-09-326-440-57
Sequence 57, Application US/09326440
Best Local Similarity 60.0k; Score 17; DB 4; Length 6;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Mueller, Anthony J.
TITLE OF INVENTION: Antisense Inhibition of Intracellular Signal
TITLE OF INVENTION: Transduction by 14-3-3-Binding Peptides
NUMBER OF SOURCES: 58
CURRENT APPLICATION DATA:
ADDRESSER: Howell & Haeferkamp, L.C.
STREET: 7733 Forsyth Boulevard, Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63105
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/336,440
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/616,669
FILING DATE:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 964064
TELEPHONE INFORMATION:
TELEPHONE: (314) 727-6032
TELEFAX: (314) 727-6032
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
SYNOPSIS:
FEATURE: Modified-site
LOCATION: 4
OTHER INFORMATION: /note="A phosphorylated serine"

US-09-326-440-57
Query Match      53.1k; Score 17; DB 4; Length 6;
Best Local Similarity 60.0k; Score 17; DB 4; Length 6;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 RARI 6
Db      1 RARI 5

RESULT 12
US-09-057-032-7
Sequence 7, Application US/09057032
Best Local Similarity 60.0k; Score 17; DB 4; Length 6;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Hubbell, Jeffrey A.

```

```

APPLICANT: Schenker, Jason
TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for
TITLE OF INVENTION: Tissue Engineering
TITLE OF INVENTION: Tissue Engineering
CORRESPONDENCE ADDRESS:
ADDRESSER: Wilson & Elkins L.L.P.
STREET: 600 Congress Avenue, Suite 2700
CITY: Austin
STATE: Texas
COUNTRY: US
ZIP: 78701
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/057,052
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,143
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Dennis L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: GAL430.21000
TELEPHONE INFORMATION:
TELEPHONE: (512) 495-8400
TELEFAX: (512) 495-8612
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
SYNOPSIS:
FEATURE:
LOCATION:
TOPOLOGY: Linear
OTHER INFORMATION:

US-09-057-052-7
Query Match      53.1k; Score 17; DB 4; Length 6;
Best Local Similarity 75.0k; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 RARI 5
Db      3 RARI 6

RESULT 13
US-09-240-514-5
Sequence 5, Application US/08240514
Best Local Similarity 75.0k; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Gopal, T. Venkat
TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
TITLE OF INVENTION: Peptide-Mediated Gene Transfer
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1400 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20005-3109
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/240,514
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
OTHER INFORMATION: /note="Peptide-Mediated Gene Transfer";
NAME: /BENT, Stephen A.

```

REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 73521/102/CLIN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)572-5348
 TELEFAX: (202)572-5399
 INVENTOR: 504136 TO NO: 5;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4 amino acids
 STRANDNESS: single
 TOPOLOGY: linear
 US-08-240-114-5

Query Match 50.0%; Score 16; DB 1; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0;

QY 1 PRAR 4
 DB 1 PRKR 4

RESULT 14
 US-08-612-302A-5

Sequence 5, Application US/08612302A
 Patent No. 5811297 5780297
 GENERAL INFORMATION:
 APPLICANT: COPAL, T Venkat
 NUMBER OF SEQUENCES: 56
 CORRESPONDENCE ADDRESS: Bastia
 STREET: One Westlake, Bastyn
 CITY: Valley Forge
 STATE: Pennsylvania
 ZIP: 19482
 COMPUTER READABLE FORM disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
 SOFTWARE: Seqman In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/612-302A
 CIRCULATION: March 1996
 CLASSIFICATION: 421
 ANNOTATED/AGENT INFORMATION:
 NAME: Azeel, Viviane 30,930
 TELEPHONE: (610) 407-0700
 TELEFAX: (610) 407-0700
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: AMBA-020
 INFORMATION FOR SEQ ID NO: 5:
 LENGTH: 4 amino acids
 STRANDNESS: n.a.
 TOPOLOGY: n.a.

Query Match 50.0%; Score 16; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0;

QY 1 PRAR 4
 DB 1 PRKR 4

RESULT 15
 US-08-637-7598-421
 Sequence 421, Application US/086377598
 Patent No. 5811297 5780297
 GENERAL INFORMATION:
 APPLICANT: David William Holden
 NUMBER OF SEQUENCES: 501
 CORRESPONDENCE ADDRESS: Rabat
 STREET: 2800 One Atlantic Center
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30309-3450
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Seqman In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/637-7598
 CIRCULATION: May 1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: PCT/GB95/02875
 FILING DATE: 11-DEC-1995
 CLASSIFICATION: 435
 ANNOTATED/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: RPMS 101
 TELEPHONE: (404) 873-8794
 TELEFAX: (404) 873-8795
 INFORMATION FOR SEQ ID NO: 421:
 LENGTH: 4 amino acids
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-637-7598-421

Query Match 50.0%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 PRAR 3
 DB 2 PRAR 4

Search completed: December 12, 2002, 15:20:53
 Job time : 12.4 secs

1 PRIOR FILING DATE: 2000-10-13
 2 NUMBER OF SEQ ID NOS: 37
 3 SOFTWARE: Patent Ver. 2.1
 4 SEQ ID NO 30
 5 LENGTH: 5
 6 TYPE: PRT
 7 ORGANISM: Artificial Sequence
 8 FEATURES:
 9 OTHER INFORMATION: Description
 10 OTHER INFORMATION: PEPTIDE
 11 US-03-977-831-30

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Query Match          56.2%; Score 18; OB 10; Length 5;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
 US-10-024-918-7
 Sequence 7, Application US/10024918
 Sequence 7, Application US/10024918
 GENERAL INFORMATION
 APPLICANT: Hubbell, Jeffrey
 APPLICANT: Schenke, Jason
 APPLICANT: Schenke, Jason
 APPLICANT: Hall, Helko
 TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
 REFERENCE: CIT 2006 CITE NO. 610/024,918
 CURRENT FILING DATE: 2006-12-18
 NUMBER OF SEQ ID NOS: 33
 SUMMARY: patent in version 3.1
 SEQ ID NO. 1
 LENGTH: 6
 TYPE: prt
 FEATURE: artificial sequence
 OTHER INFORMATION: heparin-binding sequence from fibronectin

Query Match 53.1%; Score 17; DB 9; Length 6;
Best Local Similarity 75.0%; Pred. No. 8.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 JS-09-887-469-20 *
 Application US/0987469
 Sequence 20 US/0987469
 US/0987469A
 GENERAL INFORMATION:
 APPLICANT: Kremp, Christine O.
 APPLICANT: ...
 APPLICANT: Murphy, Brian R.
 APPLICANT: Buchholz, Ursula
 APPLICANT: ...
 TITLE OF INVENTION: RESPIRATORY SYNDROMAL VIRUS VACCINES EXPRESSING
 PROTECTIVE ANTIGENS FROM PROMOTOR-PROXIMAL GENES
 CURRENT APPLICATION NUMBER: US/09/887,469
 CURRENT FILING DATE: 2001-06-22
 PRIOR APPLICATION NUMBER: US/00/621,708
 PRIOR FILING DATE: 2000-06-22
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: Patent Ver. 2.1

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: LENGTH: 6
: TYPE: PPT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Artificial
: OTHER INFORMATION: Respiratory Syncytial Virus
US-09-887-469-20

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Query Match 53.1%; Score 17; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 9.8e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-08-484-409-24
1 SEARCHED.....
2 SERIALIZED.....
3 INDEXED.....
4 FILED.....
5 MAR 17 1964
FBI - NEW YORK
PATENT NO. US2002007612A
GENERAL INFORMATION:
APPLICANT: Steinman, Lawrence
TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 52
COMPILED BY: JAMES L. HARRIS
ADDRESSSES: SEEDED AND BERRY LLP
STREET: c. 6300 Columbia Center, 701 Fifth Avenue
CITY: New York
STATE: Washington

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

US-08-484-039-34

SOFTWARE: Patent In Release 11.
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 69006
TELEPHONE:(206) 622-4900;
TELEX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE LENGTH: 4 amino acids
TYPE: amino acid
SYNOPSIS:
US-08-484-039-34 linear

Query Match 50.0%, Score
Best Local Similarity 100.0%,
Matches 3; Conservative 0; M;
4 RIV 6
1 RIV 3
RESULT 6
US-08-802-077-35
PARENT NO. US2001033842A1
GENERAL INFORMATION:
APPLICANT: Jeng-Huei Paula H.


```

; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Taylor-Fishwick, David
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/09/802.096
; CURRENT FILING DATE: 2001-03-08
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185.899
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879.495
; PRIOR FILING DATE: 1992-05-09
; PRIOR APPLICATION NUMBER: US 07/744.768
; PRIOR FILING DATE: 1991-08-14
; SEQ ID NO 1
; SEQ ID NO 21
; SEQ ID NO 38
; LENGTH: 6
; ORIGIN: Homo sapiens
; ORGANISM: Homo sapiens
US-09-802-096-21

Query Match
Best Local Similarity 50.0%; Score 16; DB 10; Length 6;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PRIORITY 6
DB 1 PRIORITY 6

RESULT 11
US-09-802-096-28
; Sequence 38, Application US/09802096
; Patent No. US200100383941
; APPLICANT: Presta, Leonard G.
; APPLICANT: Taylor-Fishwick, David
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/09/802.096
; CURRENT FILING DATE: 2001-03-08
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185.899
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879.495
; PRIOR FILING DATE: 1991-08-14
; SEQ ID NO 38
; SEQ ID NO 38
; LENGTH: 6
; ORIGIN: Homo sapiens
; ORGANISM: Homo sapiens
US-09-802-096-38

Query Match
Best Local Similarity 50.0%; Score 16; DB 10; Length 6;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PRIORITY 6
DB 1 PRIORITY 6

RESULT 12
US-09-802-096-17
; Sequence 17, Application US/10036418
; Patent No. US200201276241
; APPLICANT: Taylor-Fishwick, David
; APPLICANT: Taylor-Fishwick, David
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036.418
; CURRENT FILING DATE: 2002-01-07
; PRIOR FILING DATE: 2000-01-09
; PRIOR APPLICATION NUMBER: US 07/860.210
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 17
; SEQ ID NO 17
; LENGTH: 6
; ORIGIN: Homo sapiens
; ORGANISM: Homo sapiens
US-10-036-418-17

Query Match
Best Local Similarity 60.0%; Score 16; DB 12; Length 6;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRIORITY 5
DB 2 PSSRI 6

RESULT 13
US-10-036-418-18
; Sequence 18, Application US/10036418
; Patent No. US200201276241
; APPLICANT: Taylor-Fishwick, David
; APPLICANT: Taylor-Fishwick, David
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036.418
; CURRENT FILING DATE: 2002-01-07
; PRIOR FILING DATE: 2000-01-09
; PRIOR APPLICATION NUMBER: US 07/860.210
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 18
; SEQ ID NO 18
; LENGTH: 6
; ORIGIN: Homo sapiens
; ORGANISM: Homo sapiens
US-10-036-418-18

Query Match
Best Local Similarity 60.0%; Score 16; DB 12; Length 6;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRIORITY 5
DB 1 PSSRI 5

RESULT 14
US-10-036-10
; Sequence 10, Application US/09900936
; Patent No. US20020155141
; APPLICANT: Warthen
; APPLICANT: Warthen
; FILE REFERENCE: 00506.4
; CURRENT APPLICATION NUMBER: US/09/900.936
; CURRENT FILING DATE: 2001-07-09
; PRIOR FILING DATE: 2000-01-09
; PRIOR APPLICATION NUMBER: US 07/850.50
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 10
; SEQ ID NO 10
; LENGTH: 6
; ORIGIN: Homo sapiens
; ORGANISM: Homo sapiens
US-10-036-10

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; ORGANISM: Artificial Sequence
; FEATURE:
; DESCRIPTION: Description of Artificial Sequence:AI1 (1-4)
US-09-500-316-10

Query Match      46.9%  Score 15; DB 9; Length 4;
Best Local Similarity 46.7%; Pos=0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy  4 RIV 6
    1:1
Db   2 RVI 4

RESULT 15
US-09-771-192-10
; Sequence 10; Application US/09771192
; Patent No. US20020049162A1
; GENERAL INFORMATION:
; APPLICANT: GlaxoSmithKline
; APPLICANT: Glaxo, GSK
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; INVENTOR: GlaxoSmithKline
; CURRENT APPLICATION NUMBER: US/09771.192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOURCE: GenBank
; SEQ ID NO 10
; LENGTH: 4
; FEATURE:
; DESCRIPTION: Description of Artificial Sequence:AI1 (1-4)
US-09-771-192-10

Query Match      46.9%  Score 15; DB 10; Length 4;
Best Local Similarity 46.7%; Pos=0;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy  4 RIV 6
    1:1
Db   2 RVI 4

Search completed: December 12, 2002, 15:21:20
Job time : 6.3 secs

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R:Oseralt, R.; Oliva, R.
 Gene 133, 197-204, 1993
 C:Species: Pseudomonas syringae pv. tomato (fragment)
 A:Reference number: 137013; MUID:94040910; PMID:5224908
 A:Accession: 184439
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-4 <RES>
 A:Cross-references: EMBL:212147; NID:938134; PIDN:CM78131.1; PID:94379349

Query Watch
 Best Local Similarity 28.1%; Score 9; Da 2; Length 4;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AR 4
 II
 Db 2 AR 3

Result 15
 C41225
 copper resistance protein - Pseudomonas syringae pv. tomato (fragment)
 C:Species: Pseudomonas syringae pv. tomato
 A:Reference number: 184439; MUID:94040910; PMID:5224908
 A:Accession: C41225
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Residues: 1-5 <RES>
 A:Cross-references: EMBL:212147; NID:938134; PIDN:CM78131.1; PID:94379349
 A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer membrane proteins
 A:Accession: C41225
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: protein
 A:Residues: 1-5 <CHAS>

Query Watch
 Best Local Similarity 50.0%; Score 9; Da 2; Length 5;
 Matches 1: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PR 2
 II
 Db 2 PK 3

Search completed: December 12, 2002, 15:20:08
 Job time : 14.2 secs

GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on:

December 12, 2002, 15:14:38

Search time 7.2 Seconds
 (without alignments)
 34,504 Million cell updates/sec

Title: US-09-600-432-24

Accession score: 0.0

Sequences: 1 P84RY1 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt.40.*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	12	37.5	4	TUFT_HUMAN
2	11	34.4	5	PSK_DAUCA
3	8	28.1	4	PTFL_ANTFL
4	8	28.1	4	PTFL_ANTFL
5	7	21.9	3	TRVL_PIG
6	7	21.9	4	DCHL_PSSCH
7	7	21.9	4	PAR3_HIRBE
8	7	21.9	4	EMOL_YEAST
9	7	21.9	5	ALU4_CADMA
10	7	21.9	5	ALU4_CADMA
11	7	21.9	5	ALU4_CADMA
12	7	21.9	5	ALU4_CADMA
13	7	21.9	5	PAR3_ARTER
14	7	21.9	5	PAR3_PANMA
15	7	21.9	5	PAR3_PANMA
16	7	21.9	5	SUGA_ACHDO
17	7	21.9	5	UC22_HAZE
18	7	21.9	5	UC22_HAZE
19	7	21.9	6	CIPL_WYED
20	7	21.9	6	CIPL_WYED
21	7	21.9	6	CIPL_WYED
22	7	21.9	6	CIPL_WYED
23	7	21.9	6	CIPL_WYED
24	7	21.9	6	CIPL_WYED
25	7	21.9	6	CIPL_WYED
26	6	18.8	4	DCHL_PSSCH
27	6	18.8	4	PTFL_ANTFL
28	5	15.6	4	PTFL_ANTFL
29	5	15.6	4	PTFL_ANTFL
30	5	15.6	4	PTFL_ANTFL
31	5	15.6	4	PTFL_ANTFL
32	5	15.6	4	PTFL_ANTFL
33	5	15.6	4	PTFL_ANTFL

34 5 15.6 6 1 P84RY1
 35 4 12.5 3 1 LUXE_VIBRI
 36 4 12.5 4 1 ACHL_VIBRI
 37 4 12.5 4 1 ACHL_VIBRI
 38 4 12.5 5 1 BELT_VIBRI
 39 4 12.5 5 1 BELT_VIBRI
 40 4 12.5 5 1 BELT_VIBRI
 41 4 12.5 5 1 BELT_VIBRI
 42 3 9.4 4 1 EOXI_HUMAN
 43 3 9.4 4 1 EOXI_HUMAN
 44 3 9.4 4 1 EOXI_HUMAN
 45 3 9.4 4 1 EOXI_HUMAN

ALIGNMENTS

RESULT 1
 TUFT_HUMAN STANDARD: PRT: 4 AA.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE Phagocytosis (Rel. 10, Last annotation update)
 OS Homo sapiens (Human)
 OC Eukaryota, Metazoa, Chordata, Vertebrata, Mammalia, Homo
 CC Homo sapiens (Human)
 RN [1] UNCLC
 RX MEDLINE:72187087; PubMed:4112769;
 BA Nishio K., Constantopoulos A., Satoh P.S., Najjar V.A.;
 ET The characterization, isolation and synthesis of the phagocytosis
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
 RM [2] PROPOGOLIN CLASSE
 EX MEDLINE:6091045; PubMed:4169272;
 BA Pilsbry B.V., Najjar V.A.;
 ET The effect of leucophaenol on the lymphoid system, VI. The stimulatory
 RL effect of human polymorphonuclear leukocyte.;
 CC BIOCHEMISTRY 6:3386-3392(1967).
 CC CELL MEMBRANE OF NEUTROPHILS (IN THE RACCO, LEUCOCYTES) DURING ADHESION TO THE
 CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
 CC ACTIVITY OF NEUTROPHILS.
 DR PIR: A02147; A02147.
 DR MEM: P19100;
 DR SOURCE: 4 AA; 501 MW; 7417632IC0000000 CNE64;

Query Match 37.5% Score 12; DB 1; Length 4;
 Similarity 37.5% P84RY1.14=0;
 Mismatch 0; Mismatched 0; Gaps 0;

Oy 1 PR 2
 Db 3 PR 4

RESULT 2
 PSK_DAUCA STANDARD: PRT: 5 AA.
 AC P59261;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DE Phycoulofukine-beta (PSK-alpha) [Contains: Phycoulofukine-beta (PSK-beta)]
 CC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;

CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CNAB PERICARDIAL ORGANS.
DR PIR: A01644: HOROHA.
DR PIR: A01644: HOROHA.
KN Neuropeptide. A0411.
SQ SEQUENCE 5 AA; 649 MW; 7187673B4460000 CRC64;
Query Match 21.9%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 Y 6
DB 2 Y 2
Search completed: December 12, 2002, 15:19:17
CPU time : 8.2 secs

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]_taxid=10110;

RP SEQUENCE FROM N.A.

RC MEDLINE=1282758; PubMed=1840486;

EC Sato H., Aono S., Kashiwamata S., Kawai O.;

RA Genetic defect of Bilirubin UDP-glucuronosyltransferase in the

RT human liver. J Hepatol. 1995;24:101-106.

RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).

CC -I- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

CC EXCRETION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS.

CC -I- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR

CC EC 2.6.1.32; EC 2.6.1.33; EC 2.6.1.34; EC 2.6.1.35; EC 2.6.1.36;

CC -I- SUBCELLULAR LOCATION: MICROsome.

DR ENBL; S3836; AAB19259.1; .

FW Transferase; glycosyltransferase; Microsome; Multigene family.

FT NON-TER 4 4

SQ SEQUENCE 4 AA; 473 MW; 63732C4000000 CRC64;

Query Match 9.4%; Score 3; DB 11; Length 4;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 I 5

DB 2 V 2

RESTART 7

PRE3073

ID P83073 PRELIMINARY; FRT; 5 AA.

AC P83073-2001 (7-EMirel. 18, Created)

DT 01-OCT-2001 (7-EMirel. 18, Last sequence update)

DF 01-OCT-2001 (7-EMirel. 18, Last annotation update)

OS Bacillus cereus (Fragment).

CC Bacillus cereus.

CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

CC Bacillaceae; Bacillus.

CC [1]_taxid=1196;

RN SEQUENCE: 5 AA; 623 MW; 6801AAA3600000 CRC64;

RP SEQUENCE: 5 AA; 623 MW; 6801AAA3600000 CRC64;

RA SEQUENCE: 5 AA; 623 MW; 6801AAA3600000 CRC64;

RL Submitted (JUL-2001) to the SWISS-PROT data bank.

FW Non-TER 5 AA; 623 MW; 6801AAA3600000 CRC64;

SQ SEQUENCE 5 AA; 623 MW; 6801AAA3600000 CRC64;

Query Match 6.2%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 B 2

DB 2 K 2

RESTART 7

PRE3073

ID P83073 PRELIMINARY; FRT; 5 AA.

AC P83073-2001 (7-EMirel. 18, Created)

DT 01-OCT-2001 (7-EMirel. 18, Last sequence update)

DF 01-OCT-2001 (7-EMirel. 18, Last annotation update)

OS Bacillus cereus (Fragment).

CC Bacillus cereus.

CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

CC Bacillaceae; Bacillus.

CC [1]_taxid=1196;

RN SEQUENCE: 5 AA; 623 MW; 6801AAA3600000 CRC64;

RP SEQUENCE: 5 AA; 623 MW; 6801AAA3600000 CRC64;

RA SEQUENCE: 5 AA; 623 MW; 6801AAA3600000 CRC64;

RL Submitted (JUL-2001) to the SWISS-PROT data bank.

FW Non-TER 5 AA; 623 MW; 6801AAA3600000 CRC64;

SQ SEQUENCE 5 AA; 623 MW; 6801AAA3600000 CRC64;

Query Match 6.2%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 B 2

DB 2 K 2

Search completed: December 12, 2002, 15:18:46

Job time : 25.5 secs

dependent adhesion important in tumour cell biology

CC Claim 6; Fig 7; 47pp; English.

XX This sequence is a C-terminal tyrosine tagged peptide. This peptide

XX inhibits beta-1 integrin subunit dependent cell adhesion. Peptides

CC ANV28510-V28549 have been used to show that peptides which modulate this

CC form of cell adhesion need a C-terminal amino acid requirement, which

CC is a "lipar" motif. Studies with these peptides have also shown that

CC a "lipar" motif. Studies with these peptides have also shown that

CC the presence of the Adip motif which conveys effective beta1 integrin

CC dependent cell adhesion inhibition. The beta-1 integrin subunit dependent

CC cell adhesion and the amount is expressed on tumours such as melanoma.

CC Therefore these Lipar motif containing peptides may be important in the

CC treatment of cancer.

CC Sequence 5 AA;

CC

CC Query Match 100.0%; Score 25; DB 20; Length 5;

CC Best Local Similarity 100.0%; Prod. No. 7,8e05;

CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC

CC QY 1 RARTY 5

CC DB 1 RARTY 5

CC

CC RESULT 2

CC ID AMR19067 standard; peptide: 5 AA.

CC XX AMR19067;

CC XX Amino acid sequence of a beta1-integrin inhibitor.

CC XX Beta1-integrin inhibitor: leukocyte mediated tissue destruction;

CC XX beta1 integrin; angioplasty; surgical incision; injury-related trauma;

CC XX transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.

CC XX Synthetic.

CC XX W0200056350-A2.

CC XX

CC XX DB 28-SEP-2000.

CC XX

CC XX 22-MAR-1999; 3000W0-UG57680.

CC XX 22-MAR-1999; 99US-0125634.

CC XX 24-NOV-1999; 99US-0167538.

CC XX (MNU) UNIV MINNESOTA.

CC XX (TEBA) UNIV TEXAS SYSTEM.

CC XX (SHR) SHARON MEDICAL INC.

CC XX McCarthy JB, Milecki WJ, Jantzen GA, Low MC, Savchuk RJ;

CC XX Furcht LT;

CC XX WPI; 2000-650662/43.

CC XX Inhibition of inflammatory leukocyte mediated destruction of tissue in

CC XX a patient, comprises administering a peptide inhibitor of

CC XX beta1-integrin, useful for treatment of e.g. cancer and osteoporosis -

CC XX Claim 3; Page 38; 61pp; English.

CC XX AMR19064-67 represent beta1-integrin inhibitors. The peptides inhibit

CC beta1-integrin which is responsible for leukocyte mediated tissue

CC destruction. The peptides are useful for inhibiting inflammatory

CC leukocyte mediated destruction of tissue which occurs as a result of

CC central nervous system (CNS) ischemic injury, myocardial infarction,

CC angioplasty, surgical incisions, trauma, and related light electricity

CC and/or chemicals. They are also useful for the treatment of stroke, a

CC burn type injury, cancer, and osteoporosis.

CC Sequence 5 AA;

CC

CC Query Match 100.0%; Score 25; DB 21;

CC Best Local Similarity 100.0%; Prod. No. 7,8e05;

CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC

CC QY 1 RARTY 5

CC DB 1 RARTY 5

CC

CC RESULT 3

CC ID ANV28511 standard; peptide: 6 AA.

CC XX ANV28511;

CC XX Beta-1 Integrin cell adhesion modulator analogue #24.

CC XX 19-OCT-1999 (first entry)

CC XX Beta-1 integrin dependent cell adhesion; Lipar motif; tumour;

CC XX C-terminal tyrosine tagged; cancer; fibronectin; melanoma.

CC XX Synthetic.

CC XX W09537665-A1.

CC XX

CC XX DB 29-JUL-1999.

CC XX

CC XX 21-JAN-1999; 99W0-0801236.

CC XX 12-AUG-1998; 98US-0946312.

CC XX 22-AUG-1998; 98US-0072119.

CC XX 12-AUG-1998; 98US-0094211.

CC XX (MNU) UNIV MINNESOTA.

CC XX Brizeno A, Furcht LT, McCarthy JB;

CC XX WPI; 1995-46912/39.

CC XX New peptides modulating beta1 integrin subunit dependent cell

CC XX dependent adhesion important in tumour cell biology

CC XX Claim 6; Fig 7; 47pp; English.

CC XX This sequence is a C-terminal tyrosine tagged peptide. This peptide

CC XX inhibits beta-1 integrin subunit dependent cell adhesion. Peptides

CC XX ANV28510-V28549 have been used to show that peptides which modulate this

CC XX form of cell adhesion need a C-terminal amino acid residue (Ac) which

CC XX has a side chain including an aromatic group, and a penultimate

CC XX residue is a "lipar" motif. Studies with these peptides have also shown that

CC XX a "lipar" motif. Studies with these peptides have also shown that

CC XX inhibiting peptides do not contain D-amino acids and that it is the

CC XX dependent cell adhesion inhibition. The beta-1 integrin subunit dependent

CC XX cell adhesion is important for cell adhesion to extracellular matrix

CC XX proteins and the amount is expressed on tumours such as melanoma.

CC XX Therefore these Lipar motif containing peptides may be important in the

CC XX treatment of cancer.

CC XX Sequence 6 AA;

KW beta1-integrin; angiopathy; surgical incision; injury-related trauma;
 XX transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX Synthetic.

XX XN W020056350-A2.

XX 28-SEP-2000.

XX 22-MAR-2000; 2000MO-US07680.

XX 22-MAR-1999; 99US-0125634.

XX 24-NOV-1999; 99US-0167538.

XX (MINI) UNIV MINNESOTA.

XX (TERA) UNIV TEXAS SYSTEM.

XX (SENT) SENTINEL MEDICAL INC.

XX McCarthy JB, Mileski WJ, Jamieson GA, Low MC, Sawchuk RJ;

XX Furcht LF;

XX WPI: 2000-656062/63.

XX Inhibition of inflammatory leukocyte mediated destruction of tissue in

XX beta1-integrin mediated leukocyte mediated destruction of tissue in

XX beta1-integrin, useful for treatment of e.g. cancer and osteoporosis -

XX Claim 3; Page 38; 61pp; English.

XX AAI19051-67 represent beta1-integrin inhibitors. The peptides inhibit

XX destruction of tissue which occurs as a result of inhibiting inflammatory

XX leukocyte mediated destruction of tissue which occurs as a result of

XX central nervous system (CNS) chemically related tissue and/or infection,

XX transplant reperfusion; exposure to heat, cold, light, electricity

XX and/or chemicals. They are also useful for the treatment of stroke, a

XX burn type injury, cancer, and osteoporosis.

XX Sequence 4 AA;

XX Query Match 80.0%; Score 20; DB 21; Length 4;

XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;

XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 2 ARVY 5

XX 1 ARVY 4

XX 04-OCT-1999 (first entry)

XX Human secreted protein fragment encoded from gene 49.

XX Sequenced protein; human; treatment; diagnosis; therapy; cancer; tumor;

XX proteolytic disorder; developmental abnormality; blood disorder;

XX fetal deficiency; blood disorder; leukemia; immune system; inflammation;

XX autoimmune disease; hepatic disease; renal disease; allergy; rheumatoid;

XX cardiovascular disorder; wound healing; stroke; arthritis; obesity;

XX ashen; sepsis; acne; psoriasis; transplant rejection; infection; AIDS;

XX metabolic disorder.

XX Homo sapiens.

XX W03938681-A1.

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PD 05-AUG-1999.

XX 27-JAN-1999; 99MO-US01621.

XX 30-JAN-1998; 98US-0073170.

XX 30-JAN-1998; 98US-0073159.

XX 30-JAN-1998; 98US-0073160.

XX 30-JAN-1998; 98US-0073161.

XX 30-JAN-1998; 98US-0073162.

XX 30-JAN-1998; 98US-0073163.

XX 30-JAN-1998; 98US-0073164.

XX 30-JAN-1998; 98US-0073165.

XX 30-JAN-1998; 98US-0073167.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Carter KC, Andreas GA, Feng P, Fennie NM, Florence C;

XX Lorenz KA, Schmitt M, O, Rosen CH, Ruben SM;

XX Sappat DR, Young P, Yu G;

XX WPI: 1994-469315/39.

XX X-F280; A400458.

XX New isolated human genes and the secreted polypeptides they encode

XX useful in, e.g. treatment of Alzheimer's

XX Disclosure; Page 361; 33pp; English.

XX This invention describes novel human genes (see A4200410-200477) and the

XX secreted proteins (see A425711-255778) and fragments (see

XX A425779-725907) they encode. The polynucleotides and their corresponding

XX proteins are useful in the treatment of Alzheimer's disease and other

XX medical conditions e.g. by protein or gene therapy. Also pathological

XX conditions can be diagnosed by determining the amount of the new

XX polynucleotides and proteins in biological samples. The new

XX polynucleotides and proteins are also useful for identifying each of the 67

XX polynucleotides of the invention, based on which tissues they are most

XX representative of. The invention also provides for the diagnosis

XX of certain types of cancer, tumour neurodegenerative disorders

XX developmental abnormalities and fetal deficiencies, blood disorders,

XX autoimmune diseases, allergic diseases, autoimmune shock, Alzheimer's

XX and cognitive disorders, schizophrenia, retinosis, cardiovascular

XX disorders, wound healing, stroke, arthritis, obesity, asthma, sepsis,

XX and other diseases. The polynucleotides and proteins are also useful

XX for identifying their binding

XX partners.

XX Sequence 6 AA;

XX Query Match 76.0%; Score 10; DB 20; Length 6;

XX Best Local Similarity 76.0%; Pred. No. 7.8e+05;

XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX 2 ARVY 5

XX 1 ARVY 4

XX 26-JAN-1998 (first entry)

XX Chimeric adenovirus coat protein heparin binding motif.

XX Chimeric adenovirus; vector; coat protein; gene therapy; gene transfer;

XX human; cancer; autoimmune disease; heart disease; infection;

XX hepatitis.

XX Synthetic.

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XX W09720051-A2.
 XX PD 05-JUN-1997.
 XX XX 27-NOV-1996; 9600-US19150.
 XX XX 21-AUG-1996; 9605-0701124.
 XX PR 28-NOV-1996; 9505-0503368.
 XX PR 21-AUG-1996; 9605-0700846.
 XX XX (GENV.) GENVEC INC.
 XX PA Brough DE, Kovacs I, Micham TJ;
 XX PT WPI; 1997-110606/28.
 XX XX Adenoviral vectors containing chimeric coat protein - bind and enter
 XX cells more efficiently, useful for gene therapy of e.g. cancer,
 XX atchoume diseases, etc.
 XX PS Claim 7; Page 19; 121pp; English.
 CC This peptide is used as a universal transfer vector (UTV) sequence
 CC or as a spacer sequence in novel chimeric adenovirus coat proteins
 CC (CP), especially chimeric fibre proteins. It comprises a heparin
 CC binding domain, a chimeric CP domain, and a gene specific domain.
 CC given in AHI19810-11, AHI19813-25, AHI19827, AHI19829, AHI19831-32 and
 CC AHI19834-43). Claimed chimeric CPs differ from the w10-type CP by the
 CC presence of a spacer sequence between the CP domain and the gene
 CC in an exposed loop. This spacer sequence is located near the C-terminus or
 CC bind to and enter cells by means of a novel cell surface binding
 CC site. recombinant vectors comprising the chimeric CP are able to
 CC enter cells efficiently and bind to cells. The vectors are useful for
 CC especially at lower m.o.i. They are especially useful for gene
 CC therapy of e.g. cancers, genetic disorders, pathogenic infections,
 CC heart disease or autoimmune diseases.
 XX XX Sequence 5 AA:
 XX QWY 72.0%; Score 18; DB 18; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 RARI 4
 XX DB 2 RARI 5

Result 9
 XX ID AAT2846 standard; peptide: 5 AA.
 XX XX AAT2846;
 XX XX AAT2846;
 XX XX 19-OCT-1999 (first entry)
 XX DE Beta-1 integrin cell adhesion modulator analogue 139.
 XX XX Beta-1 integrin dependent cell adhesion: Lipar motif; tumour;
 XX C-terminal tyrosine tagged; cancer; fibronectin; melanoma.
 XX OS Synthetic.
 XX PN W09937669-A1.
 XX XX 29-JUL-1999.
 XX XX 21-JAN-1999; 9900-US261236.
 XX XX 12-AUG-1998; 9805-0062912.
 XX XX 22-JAN-1998; 9805-0072119.
 XX PR 12-AUG-1998; 9805-0056211.
 XX WPI; 2000-656062/63.
 XX Inhibition of inflammatory leukocytes mediated destruction of tissue in

(MNU) UNIV MINNESOTA.
 XX Brieno A, Pucht LT, McCarthy JB;
 XX WPI; 1999-469112/39.
 XX DR New peptides modulating beta1 integrin subunit dependent cell
 XX adhesion; useful to study cell adhesion e.g. alpha5beta1 integrin
 XX dependent adhesion important in tumour cell biology
 XX Example 11; Fig 15; 47pp; English.
 XX XX This peptide is used with AHI29510-29516 to show that peptides
 XX which mediate beta-1 integrin subunit dependent adhesion possess a
 XX C-terminal amino acid residue (AR) which has a side chain including an
 XX acidic group. They also need a penultimate C-terminal amino acid
 XX residue. Studies with these peptides have also shown that inhibiting peptides do
 XX not contain D-amino acids and that it is the presence of the ARLip motif
 XX inhibition. The beta-1 integrin subunit dependent cell adhesion is
 XX important for cell adhesion to extracellular matrix proteins, and the
 XX motif containing peptides may be important in the treatment of cancer.
 XX XX Sequence 5 AA:
 XX QWY 72.0%; Score 18; DB 20; Length 5;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 RARI 4
 XX DB 2 RARI 5

Result 10
 XX ID AAI19066 standard; peptide: 5 AA.
 XX AC AAI19066;
 XX XX 08-FEB-2001 (first entry)
 XX DE Amino acid sequence of a beta-1 integrin inhibitor.
 XX XX Beta-1 integrin inhibitor; leukocyte mediated tissue destruction;
 XX central nervous system ischemic injury; myocardial infarction;
 XX beta-1 integrin; angioplasty; surgical incision; injury related trauma;
 XX transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.
 XX OS Synthetic.
 XX XX W0200056350-A2.
 XX XX 28-SEP-2000.
 XX PD 22-MAR-2000; 2000MO-US07680.
 XX XX 22-MAR-1999; 9905-0125634.
 XX PR 24-NOV-1999; 9905-0167538.
 XX XX (MNU) UNIV MINNESOTA.
 XX XX (GENV.) GENVEC INC.
 XX PA (SENT.) SENTER MEDICAL INC.
 XX PT Pucht LT,
 XX McCarthy JB, Milecki WJ, Jamieson GA, Low MC, Sawchuk RJ;
 XX WPI; 2000-656062/63.
 XX Inhibition of inflammatory leukocytes mediated destruction of tissue in

1 REFERENCE/DOCKET NUMBER: 1991-127
 2 TELECOMMUNICATION INFORMATION:
 3 TELEPHONE: 202-783-6030
 4 TELEFAX: 202-783-6031
 5 INFORMATION FOR SEQ ID NO: 42:
 6 SEQUENCE CHARACTERISTICS:
 7 LENGTH: 5 amino acids
 8 TYPE: amino acid
 9 SYNOPSIS: single
 10 MODERATOR: none
 11 MOLECULE TYPE: peptide
 12 US-09-125-517A-42

Query Match 68.0%; Score 17; DB 3; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1,9e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RARI 4
 Db 2 RARI 5

1 RESULT 5
 2 US-09-284-625-6
 3 Sequence 6, Application US/09284625
 4 Patent No. 6087640
 5 GENERAL INFORMATION:
 6 APPLICANT: Luke, Richard William
 7 APPLICANT: Cotton, Richard
 8 FILE REFERENCE: 1991-165

9 CURRENT APPLICATION NUMBER: US/09/284,625
 10 PRIORITY CLAIMS: US-09-10-15
 11 PRIOR APPLICATION NUMBER: US/09/02817
 12 PRIOR FILING DATE: 1997-10-14
 13 PRIOR APPLICATION NUMBER: US 96218367
 14 NUMBER OF SEQ ID NOS: 30
 15 SOFTWARE: Patent Ver. 2.1
 16 SEQ ID NOS: 1-30
 17 LENGTH: 5
 18 TYPE: PPT Homo sapiens
 19 US-09-284-625-6

Query Match 68.0%; Score 17; DB 4; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1,9e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RARI 4
 Db 2 RARI 5

1 RESULT 6
 2 US-09-616-669A-57
 3 Sequence 8, Application US/0861669A
 4 Patent No. 5948765
 5 GENERAL INFORMATION:
 6 APPLICANT: Shaw, Andrew J.
 7 APPLICANT: Shaw, Andrew J.
 8 TITLE OF INVENTION: Inhibition of intracellular signal
 9 TRANSDUCTION BY 14-3-3-BINDING PEPTIDES
 10 NUMBER OF SEQUENCES: 58
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Howell & Harkamp, L.C.
 13 ATTORNEY/AGENT INFORMATION:
 14 CITY: St. Louis
 15 STATE: MO
 16 COUNTRY: U.S.A.
 17 ZIP: 63105
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk

1 COMPUTER: IBM PC compatible
 2 OPERATING SYSTEM: PC-DOS/MS-DOS
 3 SOFTWARE: Patent In Release #1.0, Version #1.30
 4 APPLICATION NUMBER: US/08/616,669A
 5 FILING DATE: 2000-AUG-19
 6 PRIORITY CLAIMS: 530
 7 ATTORNEY/AGENT INFORMATION:
 8 NAME: Holland, Donald R.
 9 TELECOMMUNICATION INFORMATION:
 10 TELEPHONE: (314) 727-5188
 11 REFERENCE/DOCKET NUMBER: 35197064
 12 US-09-125-517A-42

Query Match 68.0%; Score 17; DB 2; Length 6;
 Best Local Similarity 60.0%; Pred. No. 1,9e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RARI 5
 Db 1 RARI 5

1 RESULT 7
 2 US-09-125-517A-8
 3 Sequence 8, Application US/09125517A
 4 Patent No. 6087336
 5 GENERAL INFORMATION:
 6 APPLICANT: Cotton, Ronald
 7 APPLICANT: Edwards, Philip Neil
 8 TITLE OF INVENTION: Peptide Derivatives
 9 TRANSDUCTION BY 14-3-3-BINDING PEPTIDES
 10 NUMBER OF SEQUENCES: 62
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Figg, Ernst & Kurz, P.C.
 13 ATTORNEY/AGENT INFORMATION:
 14 CITY: Washington
 15 STATE: DC
 16 COUNTRY: U.S.A.
 17 ZIP: 20005
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk

20 SOFTWARE: Patent In Release #1.0, Version #1.30
 21 CURRENT APPLICATION DATA:
 22 APPLICATION NUMBER: US/09/125,517A
 23 FILING DATE: 2000-AUG-1994
 24 PRIORITY CLAIMS: 530
 25 APPLICATION INFORMATION:
 26 FILING DATE: 23-FEB-1996
 27 PRIOR APPLICATION DATA:
 28 FILING DATE: 05-OCT-1996
 29 ATTORNEY/AGENT INFORMATION:
 30 FILING DATE: 05-OCT-1996
 31 REGISTRATION NUMBER: 30,377
 32 REFERENCE/DOCKET NUMBER: 1991-127


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Patent No. 6800575
GENERAL INFORMATION:
  APPLICANT: Harsanyi, Hans H.
  APPLICANT: Sedlacek, Hans-Harald
  TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEINASES, AND
  CORRESPONDING ADDRESSES:
  ADDRESS: Foley & Gardner
  STREET: 3000 K Street, N.W., Suite 500
  CITY: Washington
  STATE: D.C.
  COUNTRY: USA
  ZIP: 20007-0909
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  OPERATING SYSTEM: IBM PC compatible
  SOFTWARE: PatentIn Release #1.0, Version 11.30
  CURRENT APPLICATION DATA:
  FILING DATE: 16-JAN-1998
  CLASSIFICATION: 514
  PRIORITY CLAIM: YES
  APPLICATION NUMBER: DE 197 01 141.1
  FILING DATE: 16-JAN-1997
  ATTORNEY/AGENT INFORMATION:
  NAME: Nelson, Albin J.
  REFERENCE/DOCKET NUMBER: 8648.32-US01
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 612-332-5300
  INFORMATION FOR SEQ ID NO: 33:
  SEQUENCE CHARACTERISTICS:
  TYPE: amino acid
  TOPOLOGY: linear
  MODIFICATION: none
  FRAGMENT TYPE: Peptide
  US-08-095-162-22
Query Match: 64.0% Score 16; DB 3; Length 4;
Best Local Similarity 75.0% Pred. 1; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 1;
QY 1 PART 4
DB 1 PART 4
RESULT 11
US-08-095-162-22
Sequence 22: Application US/80095162
GENERAL INFORMATION:
  APPLICANT: Wagner, Fred W.
  APPLICANT: Scout, Jay
  APPLICANT: Partidge, Bruce
  APPLICANT: Manning, Shane
  TITLE OF INVENTION: Enzymatic Method for Modification of
  CORRESPONDING ADDRESSES:
  ADDRESS: Merchant & Gould
  STREET: 3100 N. 55145th West Center
  CITY: Minneapolis
  STATE: MN
  ZIP: 55402
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  OPERATING SYSTEM: IBM PC compatible
  SOFTWARE: PatentIn Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
  FILING DATE: 06-JUN-1995
  CLASSIFICATION: 26
  PRIORITY CLAIM: YES
  APPLICATION NUMBER: US/08/470,220A
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/095,162
  FILING DATE: 30-JUL-1993
  ATTORNEY/AGENT INFORMATION:
  NAME: Nelson, Albin J.
  REFERENCE/DOCKET NUMBER: 8648.32-US01
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 612-332-5300

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COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  OPERATING SYSTEM: IBM PC compatible
  SOFTWARE: PC-DOS/MS-DOS
  CURRENT APPLICATION DATA:
  FILING DATE: 20-JUL-1993
  CLASSIFICATION: 514
  APPLICATION NUMBER: US/08/095,162
  PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 08/095,162
  FILING DATE: 30-JUL-1993
  ATTORNEY/AGENT INFORMATION:
  NAME: Nelson, Albin J.
  REFERENCE/DOCKET NUMBER: 8648.32-US01
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 612-332-5300

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1 COUNTRY: USA
 2 ZIP: 90012
 3 COMMENTS: REFERENCE FORM:
 4 MEDIUM TYPE: Floppy disk
 5 COMPUTER: IBM PC compatible
 6 SOFTWARE: SIMULINK/PSPPROG
 7 CURRENT APPLICATION DATA:
 8 RELEASE INFORMATION:
 9 RELEASE NUMBER: US/08/465/775
 10 CLASSIFICATION: 514
 11 ATTORNEY/AGENT INFORMATION:
 12 NAME: [REDACTED]
 13 REGISTRATION NUMBER: 28,215
 14 REFERENCE/DOCKET NUMBER: 1920-360
 15 TELECOMMUNICATION INFORMATION:
 16 TELEPHONE: (213) 977-1002
 17 TELEFAX: (213) 977-1003
 18 INFORMATION FOR SEQ ID NO: 10:
 19 SEQUENCE DESCRIPTION:
 20 LENGTH: 4 amino acids
 21 TYPE: amino acid
 22 MODIFICATION:
 23 MOLECULE TYPE: Peptide
 24 US-08-465-775-10

Query Match 60.08; Score 15; D8 2; Length 4;
 Best Local Similarity 66.78; Pred. No. 1.9e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 RY 5
 Db 1:1
 2 RY 4

Search completed: December 12, 2002, 15:20:53
 Job time : 9.5 secs

Genome version 5.1.3
Copyright (c) 1993 - 2002 CompuLink Ltd.
ON protein - protein search, using sw model
Run on: December 12, 2002, 15:17:24 ; Search time 5.25 Seconds
(without alignments)
13,869 Million cell updates/sec
Title: us-09-600-432-25
Sequence: 1 PART 5
Scoring table: BLASTN62
Searched: 105981 seqs, 1662342 residues
Total number of hits satisfying chosen parameters: 5573
Minimum DB seq length: 0
Maximum DB seq length: 6
Post-processing: Minimum Match 100
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6: /cpn2.6/prodata1/pubseq/US07_PUBCOMB.pep.*
7: /cpn2.6/prodata1/pubseq/US08_PUBCOMB.pep.*
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15: /cpn2.6/prodata1/pubseq/US10_PUBCOMB.pep.*

Prod. No. is the number of results predicted by chance to have a
score at least as high as the observed score. The score is printed,
and is derived by analysis of the total score distribution.

SUMMARIES						
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1	18	72.0	4	10	US-09-010-714-10	Sequence 10, Appl
2	17	68.0	6	9	US-09-900-936-9	Sequence 9, Appl
3	16	64.0	4	8	US-09-887-469-20	Sequence 20, Appl
4	16	64.0	4	8	US-08-484-408-24	Sequence 24, Appl
5	15	60.0	4	9	US-09-900-936-10	Sequence 10, Appl
6	15	60.0	4	9	US-09-900-936-10	Sequence 10, Appl
7	13	60.0	4	10	US-09-837-697A-10	Sequence 9, Appl
8	13	60.0	5	9	US-09-900-936-9	Sequence 9, Appl
9	13	60.0	5	10	US-09-771-132-9	Sequence 9, Appl
10	13	60.0	6	9	US-09-900-936-9	Sequence 9, Appl
11	13	60.0	6	9	US-09-900-936-9	Sequence 9, Appl
12	13	60.0	6	10	US-09-771-132-8	Sequence 8, Appl
13	13	60.0	6	10	US-09-771-132-8	Sequence 8, Appl
14	13	60.0	6	10	US-09-837-697A-8	Sequence 8, Appl
15	15	60.0	6	10	US-09-837-697A-8	Sequence 8, Appl
16	15	60.0	6	10	US-09-837-697A-8	Sequence 8, Appl
17	17	56.0	5	10	US-09-800-433-7	Sequence 7, Appl
18	14	56.0	5	10	US-09-800-433-7	Sequence 7, Appl
19	14	56.0	5	10	US-09-977-831-19	Sequence 19, Appl

20	14	56.0	5	10	US-09-947-387-47	Sequence 47, Appl
21	14	56.0	6	9	US-09-823-623-66	Sequence 66, Appl
22	14	56.0	6	10	US-09-904-599A-3	Sequence 3, Appl
23	14	56.0	6	10	US-09-904-599A-3	Sequence 3, Appl
24	13	52.0	4	8	US-08-484-408-11	Sequence 11, Appl
25	13	52.0	4	12	US-10-041-030-25	Sequence 25, Appl
26	13	52.0	5	10	US-09-947-387-48	Sequence 48, Appl
27	13	52.0	5	10	US-09-947-387-48	Sequence 48, Appl
28	12	48.0	4	10	US-09-941-1134-38	Sequence 38, Appl
29	12	48.0	4	10	US-09-941-1134-38	Sequence 38, Appl
30	12	48.0	5	10	US-09-837-661-28	Sequence 28, Appl
31	12	48.0	5	10	US-09-837-661-28	Sequence 28, Appl
32	12	48.0	5	10	US-09-947-387-52	Sequence 52, Appl
33	12	48.0	5	10	US-09-947-387-52	Sequence 52, Appl
34	12	48.0	5	10	US-09-947-387-127	Sequence 127, Appl
35	12	48.0	6	9	US-09-931-876-77	Sequence 77, Appl
36	12	48.0	6	9	US-09-931-876-77	Sequence 77, Appl
37	12	48.0	6	9	US-09-813-718-44	Sequence 44, Appl
38	12	48.0	6	10	US-09-207-977-91	Sequence 91, Appl
39	12	48.0	6	10	US-09-947-387-118	Sequence 118, Appl
40	12	48.0	6	10	US-09-947-387-118	Sequence 118, Appl
41	12	48.0	6	10	US-09-911-838-62	Sequence 62, Appl
42	12	48.0	6	10	US-09-911-838-62	Sequence 62, Appl
43	12	48.0	6	12	US-10-156-820-45	Sequence 45, Appl
44	11	44.0	4	9	US-09-841-730-22	Sequence 22, Appl
45	11	44.0	4	9	US-09-841-730-22	Sequence 22, Appl

ALIGNMENTS

US-09-010-714-10
 RESULT 1
 US-09-010-714-10
 Patent No. US2002001242A1
 GENERAL INFORMATION:
 APPLICANT: MCKREIN, James B.
 APPLICANT: Jids, Joid
 TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
 FILE REFERENCE: 600.332501
 CURRENT APPLICATION NUMBER: US/09/010.714
 US/09/010.714
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: Patcom Ver. 2.0
 SEQ ID NO 1
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-010-714-10

Query Match	72.0%	Score 18;	DB 10;	Length 4;
Matrix Local Similarity	100.0%;	Prod. No. 8;e+04;	Mismatches 0;	Gaps 0;
Matrix 4;	Conservative	0;	Mismatches	0;
Qy	1 PART	4		
Db	1 PART	4		
RESULT 2				
US-10-024-918-7	Appl cation US/10024918			
Sequence 7, Appl	GENERAL INFORMATION:			
APPLICANT: Hubbell, Jeffrey				
APPLICANT: Zisch, Andrea				
APPLICANT: Hall, Heike				
FILE REFERENCE: 600.332501				
CURRENT APPLICATION NUMBER: US/10/024.918				

; CURRENT FILING DATE: 2001-12-18
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1
 ; SEQUENCE: PatentIn Release #1.0, Version #1.30
 ; LENGTH: 6
 ; TYPE: PRT
 ; FEATURE: artificial sequence
 ; OTHER INFORMATION: heparin-binding sequence from fibronectin
 US-10-024-315-7

Query Match 68.0%; Score 17; DB 9; Length 6;
 Best Local Similarity 75.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RARI 4
 DB 3 RARV 6

RESULT 3
 US-09-487-469-20
 ; Sequence 20; Application US/0987469
 ; Patent No. US2001004431A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kreml, Christine D.
 ; APPLICANT: Collins, Peter L.
 ; APPLICANT: Buchholz, Ursula
 ; APPLICANT: Whitehead, Stephen S.
 ; APPLICANT: Whitehead, Stephen S.
 ; TITLE OF INVENTION: PROTECTIVE ANTIGENS FROM PROMOTOR-PROXIMAL-GENES
 ; FILE REFERENCE: 15280-424-US
 ; PRIORITY APPLICATION NUMBER: 60/0987469
 ; CURRENT FILING DATE: 2001-06-21
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIORITY FILING DATE: 2000-06-23
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; TYPE: PRT
 ; FEATURE: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: Artificial
 ; OTHER INFORMATION: Respiratory Syncytial Virus
 US-09-887-469-20

Query Match 68.0%; Score 17; DB 10; Length 6;
 Best Local Similarity 75.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RARI 4
 DB 1 RARV 4

RESULT 4
 US-09-484-409-24
 ; Sequence 24; Application US/0848409
 ; Patent No. US2001004412A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Steinman, Lawrence
 ; APPLICANT: Parvill, Scott
 ; APPLICANT: Parvill, Scott
 ; NUMBER OF INVENTIONS: 52
 ; CORRESPONDENCE ADDRESS: 52
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98104-7092

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible-POS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; APPLICANT: Kreml, Christine D.
 ; APPLICANT: Collins, Peter L.
 ; NAME: KREML, DAVID J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/OCCEP NUMBER: 690068.409C1
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INVENTION CHARACTERISTICS: 24;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-484-409-24

Query Match 64.0%; Score 16; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RIV 5
 DB 1 RIV 3

RESULT 5
 US-09-900-936-10
 ; Sequence 10; Application US/09900936
 ; Patent No. US20010055141A1
 ; APPLICANT: Rodgers, Kathleen
 ; APPLICANT: diZerega, Gene
 ; TITLE OF INVENTION: Method for Promoting Blandritic Cell Proliferation
 ; FILE REFERENCE: 00-506-A
 ; PRIORITY APPLICATION NUMBER: US/09/900,936
 ; CURRENT FILING DATE: 2001-07-09
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 4
 ; TYPE: PRT
 ; FEATURE: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: AI (1-4)
 US-09-900-936-10

Query Match 60.0%; Score 15; DB 9; Length 4;
 Best Local Similarity 66.7%; Pred. No. 8.8e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RIV 5
 DB 2 RIV 4

RESULT 6
 US-09-771-192-10
 ; Sequence 10; Application US/09771192
 ; Patent No. US2001004412A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rodgers, Kathleen
 ; APPLICANT: diZerega, Gene
 ; TITLE OF INVENTION: Method for Inhibiting Smooth Muscle Cell Proliferation
 ; FILE REFERENCE: 99-1043-A

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; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; SEQ ID NO 1: 60 04; Score 15; DB 9; Length 5;
; SOFTWARE: Patentin Ver. 2.0
; Mismatches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 10:
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: AII (1-4)
US-09-771-192-10
Query Match 60 04; Score 15; DB 10; Length 4;
Best Local Similarity 66.74; Pred No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 RY 5
DB 2 RY 4

RESULT 7
US-09-771-192-9
; Sequence 10, Application US/98837697A
; GENERAL INFORMATION:
; Patent No. US2002014682A1
; APPLICANT: Regents, Kathleen E.
; APPLICANT: Rogers, Kathleen E.
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; FILE REFERENCE: 97,017-FIA
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 10:
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: AII(1-4)
US-09-837-697A-10
Query Match 60 04; Score 15; DB 10; Length 4;
Best Local Similarity 66.74; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 RY 5
DB 2 RY 4

RESULT 8
US-09-900-936-9
; Sequence 9, Application US/9900936
; GENERAL INFORMATION:
; Patent No. US20020049162A1
; APPLICANT: Regents, Kathleen
; APPLICANT: Rogers, Kathleen
; TITLE OF INVENTION: Method for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A
; CURRENT APPLICATION NUMBER: US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9:
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: AII (1-5)
US-09-771-192-9
Query Match 60 04; Score 15; DB 9; Length 5;
Best Local Similarity 66.74; Pred No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 RY 5
DB 2 RY 4

RESULT 9
US-09-771-192-9
; Sequence 9, Application US/09771192
; GENERAL INFORMATION:
; Patent No. US20020049162A1
; APPLICANT: Regents, Kathleen
; APPLICANT: Rogers, Kathleen
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-A
; CURRENT APPLICATION NUMBER: US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9:
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: AII (1-5)
US-09-771-192-9
Query Match 60 04; Score 15; DB 10; Length 5;
Best Local Similarity 66.74; Pred No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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DB 2 RY 4

RESULT 10
US-09-837-697A-9
; Sequence 9, Application US/98837697A
; GENERAL INFORMATION:
; Patent No. US20020049162A1
; APPLICANT: University of Southern California
; APPLICANT: Rogers, Kathleen E.
; APPLICANT: diZerega, Gera
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Prolif
; FILE REFERENCE: 01-011
; CURRENT APPLICATION NUMBER: US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9:
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: AII(1-5)
US-09-837-697A-9
Query Match 60 04; Score 15; DB 10; Length 5;
Best Local Similarity 66.74; Pred No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 RY 5
DB 2 RY 4

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Best Local Similarity 66.7%; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HIT 5
DB 1 HIT 3

Search completed: December 12, 2002, 15:21:20
Job time : 5.25 secs

GenCore version 5.1.3
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OM protein - protein search, using aa model

Run on: December 12, 2002, 15:14:58 ; Search time 11 Seconds
(without alignments)
43.697 Million cell updates/sec

Title: US-09-600-432-25

Sequence score: 1

Sequence: 1 RABY 5

Scoring table: BLASTN62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: PIR-2

3: PIR-3

4: PIR-4

Pred. No. is the number of results predicted by chance to have a
score at least as good as the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Length	DB	ID	Description
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3	10	40.0	6	2	PT0870		phospholipase a2
4	10	40.0	6	2	A11490		Pyruvate kinase (E
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7	10	40.0	6	2	A11490		Pyruvate kinase (E
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9	10	40.0	6	2	A11490		Pyruvate kinase (E
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14	10	40.0	6	2	A11490		Pyruvate kinase (E
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27	10	40.0	6	2	A11490		Pyruvate kinase (E
28	10	40.0	6	2	A11490		Pyruvate kinase (E
29	10	40.0	6	2	A11490		Pyruvate kinase (E

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ALIGNMENTS

RESULT 1
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C:Species: Sus domestica (Sus domestica pig)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
Accession: S62883
PDB Locus: 342, 15-17, 1996
PDB Locus: 342, 15-17, 1996
A:Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal p
A:Accession: S62883
A:Keywords: glycoprotein; heterodimer; semen
A:Molecule type: protein
A:Residues: 1-1 <R0>
A:Keywords: glycoprotein; heterodimer; semen
Query Match 52.0% Score 13, DB 2, Length 5;
Best Local Similarity 100.0%; 28.0-0.0; Indels 0; Mismatches 0; Gaps 0;
Matches 3; Conservative 0; Indels 0; Mismatches 0; Gaps 0;

Query Match 52.0% Score 13, DB 2, Length 5;
Best Local Similarity 100.0%; 28.0-0.0; Indels 0; Mismatches 0; Gaps 0;
Matches 3; Conservative 0; Indels 0; Mismatches 0; Gaps 0;

Query Match 52.0% Score 13, DB 2, Length 5;
Best Local Similarity 100.0%; 28.0-0.0; Indels 0; Mismatches 0; Gaps 0;
Matches 3; Conservative 0; Indels 0; Mismatches 0; Gaps 0;

Query Match 52.0% Score 13, DB 2, Length 5;
Best Local Similarity 100.0%; 28.0-0.0; Indels 0; Mismatches 0; Gaps 0;
Matches 3; Conservative 0; Indels 0; Mismatches 0; Gaps 0;

Query Match 52.0% Score 13, DB 2, Length 5;
Best Local Similarity 100.0%; 28.0-0.0; Indels 0; Mismatches 0; Gaps 0;
Matches 3; Conservative 0; Indels 0; Mismatches 0; Gaps 0;

Query Match 52.0% Score 13, DB 2, Length 5;
Best Local Similarity 100.0%; 28.0-0.0; Indels 0; Mismatches 0; Gaps 0;
Matches 3; Conservative 0; Indels 0; Mismatches 0; Gaps 0;

A:Reference number: PQ0008

A:Accession: PQ0009

A:Molecule type: protein

A:Species: Streptomyces clavuligerus

A:Accession: PQ127

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 36.0% Score 9; DB 2: Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IV 5

DB 1 IV 2

RESULT 15

hypothetical 6 protein - Streptomyces clavuligerus (fragment)

C:Species: Streptomyces clavuligerus

A:Accession: PQ127

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 36.0% Score 9; DB 2: Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IV 5

DB 1 IV 2

RESULT 16

hypothetical 6 protein - Streptomyces clavuligerus (fragment)

C:Species: Streptomyces clavuligerus

A:Accession: PQ127

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 36.0% Score 9; DB 2: Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IV 5

DB 1 IV 2

RESULT 17

hypothetical 6 protein - Streptomyces clavuligerus (fragment)

C:Species: Streptomyces clavuligerus

A:Accession: PQ127

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 36.0% Score 9; DB 2: Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IV 5

DB 1 IV 2

RESULT 18

hypothetical 6 protein - Streptomyces clavuligerus (fragment)

C:Species: Streptomyces clavuligerus

A:Accession: PQ127

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 36.0% Score 9; DB 2: Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IV 5

DB 1 IV 2

Search completed: December 12, 2002, 15:20:08

Job time : 11 secs

SeqView version 5.1.3
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On protein - protein search, using w model

Run on: December 12, 2002, 15:09:54 ; Search time 21.25 seconds
48,482 million cell updates/sec

Title: us-09-600-432-25
Parient score: 25
Sequence: 1 PART 5
Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5
Searched: 671580 seps, 206047115 residues

Total number of hits satisfying chosen parameters: 7
Minimum DB seq length: 0
Maximum DB seq length: 6
Post-processing: Minimum match 0%
Maximum match 100%
Listing first 45 summaries

Database : SPTRINBL-21:
1: sp-archae:
2: sp-archae:
3: sp-fungi:
4: sp-fungi:
5: sp-human:
6: sp-human:
7: sp-ahle:
8: sp-ahle:
9: sp-phage:
10: sp-phage:
11: sp-phage:
12: sp-virus:
13: sp-vertebrate:
14: sp-vertebrate:
15: sp-unclassified:
16: sp-unclassified:
17: sp-bacteriap:
18: sp-bacteriap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	7	28.0	6	10 P82181	P82181 spinae1a ol
2	7	28.0	6	10 P82182	P82182 spinae1a ol
3	6	24.0	6	10 P82541	P82541 spinae1a ol
4	4	16.0	5	10 Q99007	Q99007 hor-deum vul
5	4	16.0	5	10 Q99007	Q99007 hor-deum vul
6	3	12.0	4	11 Q98433	Q98433 rattus norv
7	2	8.0	5	2 P83073	P83073 naclius ce

ALIGNMENTS

RESULT 1
ID P82181
AC P82181:
PRELIMINARY: PRT: 6 AA.

DT 01-JUN-2000 (TRMBUrel. 14, Created)
DT 01-MAR-2000 (TRMBUrel. 20, Last annotation update)
DT 01-MAR-2000 (TRMBUrel. 20, Last annotation update)
DE Chloroplast 508 ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Caryophyllales: Caryophyllales: Tracheophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales: Caryophyllales: Ranunculaceae; Spinacia.
NM 1137-Tairai-3592;
NM 1137-Tairai-3592;
RP SEQUENCE: ANAHO: TISSUP-10AF;
RP SEQUENCE: ANAHO: TISSUP-10AF;
PK MDLINS-20435798; PubMed-10874046;
RA Tenaquchi K., Subramanian A.R.; Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).
PL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN ENDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- FUNCTION: THIS PROTEIN ENDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
DR InterPro: IP8001790; Ribosomal_L10.
DR InterPro: IP8002163; Ribosomal_L10eub.
DR InterPro: IP8002163; Ribosomal_L10eub.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KM Ribosomal protein; Chloroplast; rRNA-binding.
SQ SEQUENCE 6 AA: 675 MW: 632184158058000 CNC64;
Query Match: Score 7, DB 10; Length 6;
Identical Similarity 33.33%; No. Gaps: 0;
Matches 1: Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Q7 1 BAR 3
D0 4 RTK 6
RESULT 2
ID P82182 PRELIMINARY: PRT: 6 AA.
AC P82182: 2000 (TRMBUrel. 14, Created)
DT 01-MAR-2000 (TRMBUrel. 20, Last annotation update)
DT 01-MAR-2000 (TRMBUrel. 20, Last annotation update)
DE Chloroplast 508 ribosomal protein L10 gamma (Fragment).
OS Rukoyota viridiplantae; Viridiplantae; Tracheophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales: Caryophyllales: Ranunculaceae; Spinacia.
NM 1137-Tairai-3592;
NM 1137-Tairai-3592;
RP SEQUENCE: ANAHO: TISSUP-10AF;
RP SEQUENCE: ANAHO: TISSUP-10AF;
PK MDLINS-20435798; PubMed-10874046;
RA Tenaquchi K., Subramanian A.R.; Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).
PL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN ENDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- FUNCTION: THIS PROTEIN ENDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
DR InterPro: IP8001790; Ribosomal_L10.
DR InterPro: IP8002163; Ribosomal_L10eub.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KM Ribosomal protein; Chloroplast; rRNA-binding.
SQ SEQUENCE 6 AA: 675 MW: 632184158058000 CNC64;
Query Match: Score 7, DB 10; Length 6;
Identical Similarity 33.33%; No. Gaps: 0;
Matches 1: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCHI_TaxID=10116:

```

ON  MODIFIED=NO)
RN  [1]

```

SEQUENCE FROM N-A

SEQUENCE FROM N. A.
STRATN=CINN.

RC STRAIN=GUNN;
PV MEDLINE=01282750; PUBMED=1040486;

RX MEDLINE=91282758; PUBMED=1840486;
RA Sato H Acno S Kuchiyama S Nakai O

SATO H., AONO S., KASHIYAMATA S., KOIWA I. O.;

Genetic defect of bilirubin UDP-glucuronosyltransferase in the

RT hyperbilirubinemic Gunn rat.⁸

RL Blochem. Biophys. Res. Commun. 177:1161-1164(1991).

CC -I- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS.

CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR

CC BETA-D-GLUCORONOSIDE,

-1- SUBCELLULAR LOCATION

EMBL: S38636; AA019259.1

[illegible]

TRANSFERASE; GLYCOSYLTRANSFERASE; MICROBOME; MUTATION

[illegible][illegible]

SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 12.0%; Score 3; DB 11; Length 4;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches	0;	Conservative	1;	Mismatches	0;	Indels	0;

Case	Age	Gender	Duration of symptoms	Family history	Genetic findings
1	25	Male	10 years	No	Normal
2	30	Female	5 years	No	Normal
3	35	Male	15 years	No	Normal
4	40	Female	20 years	No	Normal
5	45	Male	25 years	No	Normal
6	50	Female	30 years	No	Normal
7	55	Male	35 years	No	Normal
8	60	Female	40 years	No	Normal
9	65	Male	45 years	No	Normal
10	70	Female	50 years	No	Normal
11	75	Male	55 years	No	Normal
12	80	Female	60 years	No	Normal
13	85	Male	65 years	No	Normal
14	90	Female	70 years	No	Normal
15	95	Male	75 years	No	Normal

PT	dependent adhesion important in tumour cell biology	
XX	Claim 6; Fig 8; 47pp; English.	
XX	This sequence is a C-terminal tyrosine tagged peptide. This peptide	
CC	beta-1 integrin subunit dependent cell adhesion peptides	
CC	AY2810-Y2849 have been used to show that peptides which modulate this	
CC	form of cell adhesion need a C-terminal amino acid residue (Ar) which	
CC	has a side chain including an aromatic group, and a penultimate	
CC	a 'lipar' motif. Studies with these peptides have also shown that	
CC	inhibiting peptides do not contain D-amino acids and that it is the	
CC	presence of the lipid motif that conveys effective beta-1 integrin	
CC	cell adhesion is important for cell adhesion to extracellular matrix	
CC	protein, and the subunit is expressed on tumours such as melanomas.	
CC	Therefore this lipid motif containing peptides may be important in the	
CC	treatment of cancer.	
XX	Sequence 4 AA;	
XX	Query Match	
XX	Best Local Similarity 100.0%; Score 20; DB 20; Length 4;	
XX	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 ARY 4	
Db	1 ARY 4	
RESULT 2		
ID	AAI19068 standard; peptide: 4 AA.	
AC	AAI19068	
XX	08-FEB-2001 (first entry)	
XX	Amino acid sequence of a beta-1 integrin inhibitor.	
DE	Beta-1 integrin inhibitor; leukocyte mediated tissue destruction;	
XX	central nervous system ischemic injury; myocardial infarction;	
KW	beta-1 integrin; angioplasty; surgical incision; injury-related trauma;	
KW	transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.	
XX	Synthetic.	
OS		
XX	WO200056350-2.	
XX	28-SEP-2000.	
PD	PD	
XX	22-MAR-2000; 2000MO-US07680.	
XX	22-MAR-1999; 98US-019524.	
PR	24-NOV-1999; 99US-016738.	
XX	(MNU) UNIV MINNESOTA	
PA	(SINT) SINTON MEDICAL INC.	
XX	McCarthy JB, Milekai WJ, Jamieson GA, Low WC, Sawchuk NJ,	
PI	Furcht LT	
XX	WP1: 2000-055662/63.	
XX	Inhibition of inflammatory leukocyte mediated destruction of tissue in	
XX	a patient, comprises administering a peptide inhibitor of	
PT	beta-1 integrin, useful for treatment of e.g. cancer and osteoporosis -	
XX	Claim 3; page 38; 61pp; English.	
XX	AAI19054-67 represent beta-1 integrin inhibitors. The peptides inhibit	
CC	beta-1 integrin which is responsible for leukocyte mediated tissue	
CC	destruction. The peptides are useful for inhibiting inflammatory	
CC	leukocyte mediated destruction of tissue which occurs as a result of	
CC	angioplasty, surgical incisions, injury-related trauma and/or stroke,	
CC	transplant reperfusion, exposure to heat, cold, light, electricity	
CC	and/or chemicals. They are also useful for the treatment of stroke, a	
CC	burn type injury, cancer, and osteoporosis.	
XX	Sequence 4 AA;	
XX	Query Match	
XX	Best Local Similarity 100.0%; Score 20; DB 21; Length 4;	
XX	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Oy	1 ARY 4	
Db	1 ARY 4	
RESULT 3		
ID	AAI28512 standard; peptide: 5 AA.	
AC	AAI28512	
XX	19-OCT-1999 (first entry)	
DE	Beta-1 integrin cell adhesion modulator analogue #25.	
XX	Beta 1 integrin dependent cell adhesion: Lipar motif; tumour;	
KW	C-terminal tyrosine tagged; cancer; fibronectin; melanoma.	
XX	Synthetic.	
OS		
PN	WO937669-A1.	
XX	29-JUL-1999.	
XX	21-JAN-1999; 99MO-US01236.	
PF	12-AUG-1998; 98US-0056212.	
XX	22-JAN-1998; 98US-0072119.	
PR	12-AUG-1998; 98US-006211.	
XX	(MNU) UNIV MINNESOTA	
XX	Brieno A, Furcht LT, McCarthy JB,	
TI	WP1: 1999-469112/39.	
XX	New peptides modulating beta-1 integrin subunit dependent cell	
XX	adhesion useful to study cell adhesion e.g. alpha5beta1 integrin	
PT	dependent adhesion important in tumour cell biology	
XX	Claim 6; Fig 7; 47pp; English.	
XX	This sequence is a C-terminal tyrosine tagged peptide. This peptide	
XX	AY2810-Y2849 have been used to show that peptides which modulate this	
CC	form of cell adhesion need a C-terminal amino acid residue (Ar) which	
CC	has a side chain including an aromatic group, and a penultimate	
CC	C-terminal amino acid residue (Ar) with a 'lipar' motif, i.e.	
CC	a 'lipar' motif. Studies with these peptides have also shown that	
CC	inhibiting peptides do not contain D-amino acids and that it is the	
CC	presence of the lipid motif that conveys effective beta-1 integrin	
CC	dependent cell adhesion inhibition. The beta-1 integrin subunit dependent	
CC	cell adhesion is important for cell adhesion to extracellular matrix	
CC	protein, and the subunit is expressed on tumours such as melanomas.	
CC	Therefore this lipid motif containing peptides may be important in the	
CC	treatment of cancer.	
XX	Sequence 5 AA;	

Query Match	100.0%; Score 20; DB 20; Length 5;	
Best Local Similarity	100.0%; Pred. No. 7,8e05;	
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AR1Y 4	
	2 AR1Y 5	
DB		
RESULT 4		
AA19067		
ID	AA19067 standard; peptide: 5 AA.	
AC	AA19067	
DE	08-FEB-2001 (first entry)	
XX	Amino acid sequence of a beta-integrin inhibitor.	
XX	Beta-1 integrin inhibitor; leukocyte mediated tissue destruction;	
XX	central nervous system ischemic injury; myocardial infarction;	
XX	beta-1 integrin; angioplasty; surgical incision; injury-related trauma;	
XX	transplant reperfusion; stroke; burn type injury; cancer; osteoporosis.	
OS	Synthetic.	
XX	W0200056350-A2.	
XX	W0200056350-A2.	
XX	28-SEP-2000.	
XX	22-MAR-1999; 200000-0807680.	
XX	24-MAR-1999; 9908-0125634.	
XX	24-MAR-1999; 9908-0107538.	
PA	(MIMU) UNIV MINNESOTA.	
DA	(SIRT) SENTERON MEDICAL INC.	
PI	McCarthy JB, Milenki WJ, Jamerson GA, Low WC, Sawchuk RJ;	
PI	Furcht LJ;	
XX	WPI: 2000-65662/63.	
XX	Inhibition of inflammatory leukocyte mediated destruction of tissue in	
XX	a patient, comprises administering a peptide inhibitor of	
XX	beta-1 integrin. useful for treatment of e.g. cancer and osteoporosis -	
XX	Claim 3; Page 38; 61pp: English.	
CC	AA19064-67 represent beta-1 integrin inhibitors. The peptides inhibit	
CC	beta-1 integrin which is responsible for leukocyte mediated tissue	
CC	destruction. The peptides are useful for inhibiting inflammatory	
CC	conditions associated with beta-1 integrin, including myocardial infarction,	
CC	central nervous system (CNS) ischemic injury, myocardial infarction,	
CC	angioplasty, surgical incisions, injury-related trauma, and/or	
CC	osteoporosis. The peptides are also useful for inhibiting light, electricity	
CC	and/or chemicals. They are also useful for the treatment of stroke, a	
CC	burn type injury, cancer, and osteoporosis.	
XX	Sequence 5 AA.	
XX	Sequence 5 AA:	
XX	Query Match	100.0%; Score 20; DB 21; Length 5;
XX	Best Local Similarity	100.0%; Pred. No. 7,8e05;
XX	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AR1Y 4	
	11111	
DB	2 AR1Y 5	
RESULT 5		
AA19511		
ID	AA19511 standard; peptide: 6 AA.	
AC	AA19511	
DE	19-OCT-1999 (first entry)	
XX	Beta-1 integrin cell adhesion modulator analogue #24.	
XX	Beta-1 integrin dependent cell adhesion; LIPAP motif; tumour;	
XX	C-terminal tyrosine tagged; cancer; fibronectin; melanoma.	
OS	Synthetic.	
XX	W09937669-A1.	
XX	29-JUL-1999.	
XX	21-JAN-1999; 9900-0801236.	
XX	12-AUG-1998; 9805-0096212.	
XX	12-AUG-1998; 9805-0096212.	
XX	12-AUG-1998; 9805-0096211.	
XX	(MIMU) UNIV MINNESOTA.	
PI	Brienza A, Furcht LJ, McCarthy JB;	
XX	WPI: 1999-469112/39.	
XX	New peptides modulating beta1 integrin submit dependent cell	
XX	adhesion. useful to study cell adhesion e.g. alpha/beta1 integrin	
XX	dependent adhesion important in tumour cell biology	
XX	Claim 6; Fig 7: 47pp: English.	
CC	This sequence is a C-terminal tyrosine tagged peptide. This peptide	
CC	inhibits beta-1 integrin submit dependent cell adhesion. Peptides	
CC	modulate the interaction between the submit and the peptides which modulate this	
CC	form of cell adhesion need a C-terminal unpaired amino acid which	
CC	has a side chain including an aromatic group, and a penultimate	
CC	amino acid which is a tyrosine. The peptides are useful for inhibiting	
CC	a 'lipar' motif. Studies with the peptides have shown that the	
CC	inhibiting peptides do not contain tyrosine acids and that it is the	
CC	presence of the Artp motif that conveys effective beta1 integrin	
CC	inhibition. The peptides are useful for inhibiting cell adhesion	
CC	cell adhesion is important for cell adhesion to extracellular matrix	
CC	proteins, and the submit is expressed on tumours such as melanoma.	
CC	and the submit motif containing peptides may be important in the	
CC	treatment of cancer.	
XX	Sequence 6 AA:	
XX	Query Match	100.0%; Score 20; DB 20; Length 6;
XX	Best Local Similarity	100.0%; Pred. No. 7,8e05;
XX	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AR1Y 4	
	11111	
DB	3 AR1Y 6	
RESULT 6		
AA19065		
ID	AA19065 standard; peptide: 6 AA.	
AC	AA19065	
DE	08-FEB-2001 (first entry)	
XX	Amino acid sequence of a beta-1 integrin inhibitor.	
XX	Beta-1 integrin inhibitor; leukocyte mediated tissue destruction;	
XX	central nervous system ischemic injury; myocardial infarction.	

PR 21-NOV-1994: 943P-0286517.
 XX 21-NOV-1994: 943P-031185.
 PA (KIRI) KIRIN BEER KK.
 XX WPI, 1996-040671/05.
 XX Sulfolobus spp. derived transferase and amylase - for production of
 XX alpha, alpha-trehalose from malto-oligosaccharides(s)
 XX Example 1-11; Page 179; 357pp; Japanese.
 XX ARS90552-54 are Arg-N peptide fragments of a transference isolated from
 XX Sulfolobus acidocaldarius. The transference (ARS90513) acts on
 XX saccharides having at least three sugar units, in which at least three
 XX units are alpha-1,4 linked, to transform the
 XX alpha-1,4 linkage to alpha-1,6 linkage.
 XX mol. wt. of 74 to 76 kDa. It is characterized by working at pH 4.5-6.0
 XX and at 90 deg C. It has an isoelectric point of 5.3-6.3 and retains
 XX activity in the presence of 5 mM copper sulphate. Use of the transference and an enzyme
 XX inhibited by 5 mM copper sulphate. Use of the transference and an enzyme
 XX in succession on suitable substrates such as malto-oligosaccharides, is
 XX useful for the production of alpha, alpha-trehalose.
 XX Sequence 6 AA:
 SQ
 Query Match 85.0%; Score 17; DB 19; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AR1Y 4
 DB 3 SR1Y 6
 RES027 13
 XX ANK56544
 XX ID ANK56544 standard; peptide; 6 AA.
 XX ANK5644;
 XX 28-JUL-1998 (first entry)
 DE Enzyme inhibitor peptide SEQ ID NO:145.
 DT
 XX Enzyme inhibitor: t-PA, u-PA; chymotrypsin; serine protease; active;
 XX Enzyme inhibitor: t-PA, u-PA; chymotrypsin; serine protease; active;
 XX Identification: Kinase; phosphatase; serpin.
 XX Homo sapiens.
 XX M09747314-A1.
 XX 18-DEC-1997.
 XX 10-JUN-1997; 97MO-0509760.
 XX 10-JUN-1996; 960S-0019495.
 XX (SCRI) SCHIFFERS RES INST.
 XX Ke S, Madison IL;
 XX WPI, 1996-062746/06.
 XX Substrate-subtraction phase display peptide libraries - used to
 XX identify the amino acid sequence of an immunogen and used for
 XX modulating the immune system.
 XX Disclosure; : 7pp; English.
 XX Claim 25; Page 09; 198pp; English.
 XX The present sequence represents an enzyme inhibitor peptide used in
 XX the method of the invention to distinguish between t-PA and u-PA. The

CC Present invention describes a substrate subtraction library for the
 CC identification of peptide substrates selective between a first enzyme
 CC (E1) and a second enzyme (E2), comprising a collection different
 CC of peptide substrates selective between a first enzyme (E1) and a second enzyme
 CC (E2). Also described are: (1) a method (M1) for identifying peptide
 CC substrates selective between a first enzyme (E1) and a second enzyme
 CC identified by M1; (3) a polypeptide for identifying a peptide
 CC comprising one of 237 amino acid sequences (see AM556801 to AM55947,
 CC and AM55949 to AM57039); (4) a recombinant DNA vector comprising DNA
 CC encoding the polypeptide of (3); (5) a recombinant cell containing the
 CC the M1; (5) a prokaryotic or eukaryotic cell containing the vector of
 CC (4); (6) an antibody (Ab) immunoreactive with at least one of the
 CC between active and latent forms of proteases inhibiting between active and
 CC (between active and latent forms of proteases inhibiting between active and
 CC phosphatases of enzyme inhibitors, e.g., proteases, kinases and
 CC peptides and in the identification of naturally occurring protease
 CC inhibitors; Enzyme-inhibiting peptides identified can be used to treat a
 CC serpin deficiency or a disorder of serine processes.
 XX Sequence 6 AA:
 SQ
 Query Match 85.0%; Score 17; DB 19; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AR1Y 4
 DB 2 ARH 5
 RES018 14
 XX APP1620
 XX ID APP1620 standard; protein; 4 AA.
 XX APP1620.
 XX 09-JUL-1990 (first entry)
 DT
 XX Motif useful in tolerization alone or in association with antigens to
 XX peripheral nervous system myelin protein, a proteolipid protein, a PNS and
 XX CNS myelin constituent and the acetyl choline receptor.
 XX Antigen: MBP; myelin basic protein; transmembrane antigen;
 XX myasthenia gravis; myasthenics; Transplantation antigen.
 XX Synthetic.
 XX EP04279-A.
 XX 22-FEB-1989.
 XX 17-AUG-1988; 88EP-0307608.
 XX 17-AUG-1988; 88US-0086594.
 XX (STFD) LELAND STANFORD JR UNIV.
 XX Steilman L;
 XX WPI; 1989-055656/08.
 XX Oligopeptide and polypeptide compounds -
 XX based on the amino acid sequence of an immunogen and used for
 XX modulating the immune system.
 XX Disclosure; : 7pp; English.
 XX Sequences will normally be part of 9-15 amino acid sequence, excluded as
 XX motifs for immunisation but useful in tolerisation..

```

SQ Sequence 4 AA;
Query Match Score 16; DB 10; Length 4;
Local Similarity 100.0%; First Residue 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 R1Y 4
   1 11
DB 1 R1Y 3

RESULT 15
AAW5761 standard; peptide; 4 AA.
XX AAW5761;
AC AAW5761;
XX
XX 08-JUL-1998 (first entry)
DE Immunisation motif associated with P2 8.
KW Myelin basic protein; Immunity; Immune response; neurological; T-cell;
KW myelin; Immunogen; B-cell; transplantation antigen; immunomodulator.
OS Unidentified.
XX
XX EP805162-AL.
FN
PD 05-NOV-1997.
XX
XX 17-AUG-1988; 88EP-0307608.
XX
PR 17-AUG-1987; 87US-0086694.
XX
XX
PA (SYND ) UNIV LELAND STANFORD JUNIOR.
XX
XX Steinman L, Zamvil S;
XX
XX Polyptide comprising human myelin basic protein fragment - useful
XX as immuno modulator
XX
XX Disclosure; Page 8; Spp: English.
CC The present sequence represents an immunisation motif normally excluded,
CC but which may be used with advantage for tolerisation by itself or in
CC combination with other immunisation motifs. The present invention
CC describes a polypeptide comprising a human myelin basic
CC protein (MBP) fragment including 89-101 of MBP, excluding native MBP.
CC The polypeptide is useful for inducing an immune response in
CC 89-101 of MBP. The polypeptide can be used for tolerising a mammalian
CC host immune system comprising B and T cells to an immunogen of interest,
CC wherein said immunogen is restricted by a transplantation antigen of said
CC host.
XX
XX Sequence 4 AA;
Query Match Score 16; DB 19; Length 4;
Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 R1Y 4
   1 11
DB 1 R1Y 3

Search completed: December 12, 2002, 15:17:16
Job time : 22.6 secs

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; Sequence 10, Application US/09245680B
; Patent No. 6239109
; Title: Artificial Sequence
; APPLICANT: Rodgers, Kathleen
; FILER REFERENCE: 980098
; FILE REFERENCE: 980098 Method of Promoting Erythropoiesis
; CURRENT APPLICATION NUMBER: US/09/745,680B
; CURRENT FILING DATE: 1999-02-08
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-4)
US-09-245-680-10

Query Match
Best Local Similarity 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RV 4

RESULT 6
; Sequence 10, Application US/09198060C
; Patent No. 6248587
; Title: Artificial Sequence
; APPLICANT: Rodgers, Kathleen
; FILER REFERENCE: 97,017-F1
; FILE REFERENCE: 97,017-F1
; CURRENT APPLICATION NUMBER: US/09/198,806C
; CURRENT FILING DATE: 1998-11-24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-4)
US-09-198-806C-10

Query Match
Best Local Similarity 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RV 4

RESULT 7
; Sequence 10, Application US/09352191
; Patent No. 6357770
; Title: Artificial Sequence
; APPLICANT: Rodgers, Kathleen
; FILER REFERENCE: 98165B
; FILE REFERENCE: 98165B
; CURRENT APPLICATION NUMBER: US/09/352,191
; CURRENT FILING DATE: 1999-07-12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-4)
US-09-352-191-10

Query Match
Best Local Similarity 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RV 4

RESULT 8
; Sequence 10, Application US/09012400D
; Patent No. 6455510
; Title: Artificial Sequence
; APPLICANT: Rodgers, Kathleen
; FILER REFERENCE: 97,017-G
; FILE REFERENCE: 97,017-G
; CURRENT APPLICATION NUMBER: US/09/012,400D
; CURRENT FILING DATE: 1998-01-23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-4)
US-09-012-400-10

Query Match
Best Local Similarity 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RV 4

RESULT 9
; Sequence 10, Application US/09244563A
; Patent No. 6455510
; Title: Artificial Sequence
; APPLICANT: Rodgers, Kathleen
; FILER REFERENCE: 97017K1
; FILE REFERENCE: 97017K1
; CURRENT APPLICATION NUMBER: US/09/244,563A
; CURRENT FILING DATE: 1999-03-08
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-4)
US-09-244-563-10

Query Match
Best Local Similarity 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RV 4

RESULT 10
; Sequence 10, Application US/09244563A
; Patent No. 6455510
; Title: Artificial Sequence
; APPLICANT: Rodgers, Kathleen
; FILER REFERENCE: 97017K1
; FILE REFERENCE: 97017K1
; CURRENT APPLICATION NUMBER: US/09/244,563A
; CURRENT FILING DATE: 1999-03-08
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-4)
US-09-244-563-10

Query Match
Best Local Similarity 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RV 4

```

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QY 2 RY 4
DB 2 RY 4

US-08-465-775-9
RESULTS 10
US-08-465-775-9
Patent No. 5955430
GENERAL INFORMATION:
APPLICANT: Spilals, Kathleen E.
TITLE OF INVENTION: USE OF ANGIOSTENIN II FRAGMENTS AND
SEQUENCE CHARACTERISTICS: 14
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O Robbins
ADDRESS: 20155445th Avenue Street #500
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90012
COMPUTER READABLE FORM:
COMPUTER TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/465,775
FILING DATE: 08-514
PRIORITY DATE: 08-514
ATTORNEY/AGENT INFORMATION:
NAME: Spilals, John P.
REFERENCE/DOCKET NUMBER: 1320-360
TELEPHONE: (213) 971-0001
TELEFAX: (213) 971-0001
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TOPOLOGY: linear
US-08-465-775-9
Query Match Similarity 75.0%; Score 15; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RY 4

US-08-465-586-58
RESULTS 11
US-08-465-586-58
Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: David Tilson
TITLE OF INVENTION: PRIORITIZED AND RECOMBINANT ANTIGENIC
SEQUENCE CHARACTERISTICS: 14
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
ADDRESS: 1110 Broadway at the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
COMPUTER TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/465,586
FILING DATE: 08-514
PRIORITY DATE: 08-514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REFERENCE/DOCKET NUMBER: 0575/43862-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 931-0524
TELEFAX: (213) 931-0524
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDNESS: single
MOLECULE TYPE: protein
US-08-465-586-58
Query Match Similarity 75.0%; Score 15; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 1 RY 3

US-09-208-337-9
RESULTS 12
US-09-208-337-9
Patent No. 6048704
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
TITLE OF INVENTION: USE OF ANGIOSTENIN II FRAGMENTS
SEQUENCE CHARACTERISTICS: 15
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kobbie Martens, Olson & Bear
ADDRESS: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: U.S.A.
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
COMPUTER TYPE: Diskette
OPERATING SYSTEM: Windows
SOFTWARE: PatSeq for Windows Version 2.0
APPLICATION NUMBER: US/09/208,337
FILING DATE: 09-09/208,337
PRIORITY DATE: 09-09/208,337
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/465,775
FILING DATE: 08-JUN-1995
APPLICATION NUMBER: 08/337,781
PRIORITY DATE: 08-JUN-1995
APPLICATION NUMBER: 08/126,368
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rodgers, Kathleen
REFERENCE/DOCKET NUMBER: USC010.001C2
TELEPHONE: 949-760-0404
TELEFAX: 949-760-9502

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1  TELEX:
2  INFORMATION FOR SEQ ID NO: 9:
3  SOURCE: CHEMICAL ABSTRACTS
4  LENGTH: 5 amino acids
5  TYPE: amino acid
6  SYNOPSIS: single
7  ZEPHYRUS: single
8  MOLECULE TYPE: Peptide
9
10 US-09-208-337-9
11
12 Query Match
13 Best Local Similarity 75.0%; Score 15; DB 3; Length 5;
14 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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16 Qy 2 RY 4
17 Db 2 RY 4
18
19 RESULT 13
20 US-09-990-664-10
21 Sequence 10, Application US/08990664
22 GENERAL INFORMATION:
23 APPLICANT: Rodgers, Kathleen
24 APPLICANT: dizerega, Gare
25 TITLE OF INVENTION: IN SKIN GRAFTS
26 NUMBER OF SEQUENCES: 46
27 CURRENT FILING DATE: 1999-02-08
28 ADDRESS: 620 Newport Center Drive 16th Floor
29 CITY: Newport Beach
30 STATE: CA
31 COUNTRY: U.S.A.
32 ZIP: 92660
33 COMPUTER: IBM Compatible
34 MEDIUM TYPE: Diskette
35 NAME: Alton, Daniel S. 115
36 NAME: Alton, Daniel S. 115
37 REFERENCE/DOCKET NUMBER: USC012 001A
38 TELECOMMUNICATION INFORMATION:
39 REFERENCE/DOCKET NUMBER: USC012 001A
40 TELEPHONE: 714-760-5502
41
42 TELER:
43 INFORMATION FOR SEQ ID NO: 10:
44 LENGTH: 5 amino acids
45 TYPE: amino acid
46 MOLECULE TYPE: Peptide
47
48 US-09-990-664-10
49
50 Query Match
51 Best Local Similarity 75.0%; Score 15; DB 3; Length 5;
52 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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54 Qy 2 RY 4
55 Db 2 RY 4
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57 RESULT 14
58 US-09-373-962-9
59 Sequence 10, Application US/09373962
60 GENERAL INFORMATION:
61 APPLICANT: Rodgers, Kathleen
62 APPLICANT: dizerega, Gare
63 TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
64 CURRENT FILING DATE: 1999-08-13
65 ADDRESS: 620 Newport Center Drive 16th Floor
66 CITY: Newport Beach
67 STATE: CA
68 COUNTRY: U.S.A.
69 ZIP: 92660
70 COMPUTER: IBM Compatible
71 MEDIUM TYPE: Diskette
72 NAME: Alton, Daniel S. 115
73 NAME: Alton, Daniel S. 115
74 REFERENCE/DOCKET NUMBER: USC012 001A
75 TELECOMMUNICATION INFORMATION:
76 REFERENCE/DOCKET NUMBER: USC012 001A
77 TELEPHONE: 714-760-5502
78
79 TELER:
80 INFORMATION FOR SEQ ID NO: 10:
81 LENGTH: 5 amino acids
82 TYPE: amino acid
83 MOLECULE TYPE: Peptide
84
85 US-09-373-962-9
86
87 Query Match
88 Best Local Similarity 75.0%; Score 15; DB 4; Length 5;
89 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
90
91 Qy 2 RY 4
92 Db 2 RY 4
93
94 RESULT 15
95 US-09-445-680-9
96 Sequence 10, Application US/09445680
97 GENERAL INFORMATION:
98 APPLICANT: Rodgers, Kathleen
99 APPLICANT: dizerega, Gare
100 TITLE OF INVENTION: Method of Promoting Erythropoiesis
101 CURRENT FILING DATE: 1999-02-08
102 ADDRESS: 620 Newport Center Drive 16th Floor
103 CITY: Newport Beach
104 STATE: CA
105 COUNTRY: U.S.A.
106 ZIP: 92660
107 COMPUTER: IBM Compatible
108 MEDIUM TYPE: Diskette
109 NAME: Alton, Daniel S. 115
110 NAME: Alton, Daniel S. 115
111 REFERENCE/DOCKET NUMBER: USC012 001A
112 TELECOMMUNICATION INFORMATION:
113 REFERENCE/DOCKET NUMBER: USC012 001A
114 TELEPHONE: 714-760-5502
115
116 TELER:
117 INFORMATION FOR SEQ ID NO: 10:
118 LENGTH: 5 amino acids
119 TYPE: amino acid
120 MOLECULE TYPE: Peptide
121
122 US-09-445-680-9
123
124 Query Match
125 Best Local Similarity 75.0%; Score 15; DB 4; Length 5;
126 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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128 Qy 2 RY 4
129 Db 2 RY 4
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131 Job completed: December 12, 2002, 15:20:54
132 Job time : 8.6 secs

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:17:24 ; Search time 4.2 Seconds
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Title: us-09-600-432-26

Sequences: 1 PART 4

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Gapop 10.0 , Gapext 0.5

Searched: 10591 seqs, 1662342 residues

Total number of hits satisfying chosen parameters: 5973

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Listing First 45 summaries

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- 3: /csp2.5/pdata1/pubpaas/US06_NEW_PUB pep.*
- 4: /csp2.5/pdata1/pubpaas/US05_NEW_PUB pep.*
- 5: /csp2.5/pdata1/pubpaas/US04_NEW_PUB pep.*
- 6: /csp2.5/pdata1/pubpaas/US03_NEW_PUB pep.*
- 7: /csp2.5/pdata1/pubpaas/US02_NEW_PUB pep.*
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- 10: /csp2.5/pdata1/pubpaas/US00_NEW_PUB pep.*
- 11: /csp2.5/pdata1/pubpaas/US10_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a
minimum match of the specified length. The results are sorted
and is derived by analysis of the local score distribution.

SUMMARIES

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1	16	86.0	4	8	US-08-484-409-24
2	15	75.0	4	9	US-09-900-936-10
3	15	75.0	4	10	US-09-900-936-9
4	15	75.0	4	10	US-09-937-697A-10
5	15	75.0	5	9	US-09-900-936-9
6	15	75.0	5	10	US-09-937-697A-10
7	15	75.0	5	10	US-09-937-697A-9
8	15	75.0	6	9	US-09-900-936-5
9	15	75.0	6	10	US-09-937-697A-8
10	15	75.0	6	10	US-09-937-697A-5
11	15	75.0	6	10	US-09-937-697A-8
12	15	75.0	6	10	US-09-937-697A-5
13	15	75.0	4	8	US-08-484-409-31.8
14	13	65.0	4	10	US-09-410-714-10
15	13	65.0	4	10	US-09-410-714-10
16	13	65.0	4	10	US-09-410-714-10
17	13	65.0	4	10	US-09-410-714-10
18	12	60.0	4	10	US-09-947-387-48
19	12	60.0	5	10	US-09-947-387-47

20	12	60.0	5	10	US-09-947-387-92
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22	12	60.0	5	10	US-09-947-387-127
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24	12	60.0	6	9	US-09-947-387-127
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26	12	60.0	6	10	US-09-947-387-118
27	12	60.0	6	10	US-09-947-387-118
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39	11	55.0	4	10	US-09-769-145-58
40	11	55.0	4	10	US-09-769-145-58
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42	11	55.0	5	9	US-10-014-485A-63
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45	11	55.0	5	10	US-09-413-653-8

ALIGNMENTS

RESULT 1
US-08-484-409-24
Sequence 24, App1
Sequence 24, App1
GENERAL INFORMATION:
APPLICANT: Steinman, Lawrence
TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 52
COMPARISON METHOD: BLAST
COMPARISON PROGRAM: BLAST
ADDRESS: SEED MEDICAL
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMMENTS: BLAST RESULTS
MEDIUM TYPE: Plasmid
COMPUTER: IBM PC compatible
SERIALS SYSTEM: PC DOS/MS-DOS
SOFTWARE: BLAST, Version 1.6.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,409
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 690066 409C1
TELEPHONE: (206) 682-6031
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear

Query Match 80.0% Score 16 DB Seq Length 4;
Best Local Similarity 100.0% Pred. No. 8.8e+04

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIV 4
Db 1 RIV 3

RESULT 2
US-09-900-936-10

; Sequence 10; Application US/0900936
; Heat Local Similarity 66.78; Pred. No. 8.8e+04;
; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A; US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 1: Patent Ver. 2.0
; LENGTH: 4
; TYPE: RPT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI (1-4)
US-09-900-936-10

Query Match 75.0%; Score 15; DB 10; Length 4;
Heat Local Similarity 66.78; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIV 4
Db 2 RIV 4

RESULT 3
US-09-771-192-10

; Sequence 9; Application US/09771192
; Heat Local Similarity 75.0%; Score 15; DB 9; Length 4;
; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-B; US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 1: Patent Ver. 2.0
; LENGTH: 4
; TYPE: RPT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI (1-4)
US-09-771-192-10

Query Match 75.0%; Score 15; DB 10; Length 4;
Heat Local Similarity 75.0%; Score 15; DB 9; Length 4;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIV 4
Db 2 RIV 4

RESULT 4
US-09-837-697A-10

; Sequence 9; Application US/09837697A
; Heat Local Similarity 75.0%; Score 15; DB 9; Length 4;
; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; TITLE OF INVENTION: Methods for Promoting Hematopoietic and Mesenchymal Cell Prolif

; APPLICANT: University of Southern California
; APPLICANT: diffeys, Gerg
; TITLE OF INVENTION: Methods for Promoting Hematopoietic and Mesenchymal Cell Prolif

; FILE REFERENCE: 97-017-F1A US/09/837,697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1: Patent Ver. 2.0
; LENGTH: 4
; TYPE: RPT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: AI(1-4)
US-09-837-697A-10

Query Match 75.0%; Score 15; DB 10; Length 4;
Heat Local Similarity 66.78; Pred. No. 8.8e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIV 4
Db 2 RIV 4

RESULT 5
US-09-900-936-9

; Sequence 9; Application US/0900936
; Heat Local Similarity 75.0%; Score 15; DB 9; Length 4;
; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; FILE REFERENCE: 00-506-A; US/09/900,936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 1: Patent Ver. 2.0
; LENGTH: 5
; TYPE: RPT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI (1-5)
US-09-900-936-9

Query Match 75.0%; Score 15; DB 9; Length 5;
Heat Local Similarity 75.0%; Score 15; DB 9; Length 5;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIV 4
Db 2 RIV 4

RESULT 6
US-09-771-192-9

; Sequence 9; Application US/09771192
; Heat Local Similarity 75.0%; Score 15; DB 9; Length 4;
; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; GENERAL INFORMATION:
; APPLICANT: diffeys, Gerg
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 99-1043-B; US/09/771,192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 1: Patent Ver. 2.0
; LENGTH: 5
; TYPE: RPT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI (1-5)
US-09-771-192-9

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; TYPE: PRT
; FEATURES: Artificial Sequence
; PATENT: US20020165141
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-5)

Query Match
Best Local Similarity 75.0%; Score 15; DB 10; Length 5;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RY 4

RESULT 7
US-09-437-697A-9
; Sequence 9, Application US/09837697A
; Patent No. US20020165141
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; APPLICANT: Rogers, Kathleen E.
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell Proliferation
; TITLE OF INVENTION: Differentiation
; CURRENT APPLICATION NUMBER: US/09/437 697A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 9 PatentIn version 3.1
; LENGTH: 5
; SEQ ID NO 9
; FEATURE:
; ORGANISM: Artificial sequence
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-5)
US-09-437-697A-9

Query Match
Best Local Similarity 75.0%; Score 15; DB 10; Length 5;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RY 4

RESULT 8
US-09-900-936-5
; Sequence 8, Application US/0900936
; Patent No. US20020165141
; GENERAL INFORMATION:
; APPLICANT: diferega, Gere
; APPLICANT: diferega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; TITLE OF INVENTION: or Differentiation
; CURRENT APPLICATION NUMBER: US/09/900.936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 5
; SEQ ID NO 5
; FEATURE:
; ORGANISM: Artificial Sequence
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (2-7)
US-09-900-936-5

Query Match
Best Local Similarity 75.0%; Score 15; DB 9; Length 6;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 1 RY 3

RESULT 11
US-09-900-936-8
; Sequence 8, Application US/0900936
; Patent No. US20020165141
; GENERAL INFORMATION:
; APPLICANT: diferega, Gere
; APPLICANT: diferega, Gere
; TITLE OF INVENTION: Methods for Promoting Dendritic Cell Proliferation
; TITLE OF INVENTION: or Differentiation
; CURRENT APPLICATION NUMBER: US/09/900.936
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 8
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 8
; SEQ ID NO 8
; FEATURE:
; ORGANISM: Artificial Sequence
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (1-6)
US-09-900-936-8

Query Match
Best Local Similarity 75.0%; Score 15; DB 9; Length 6;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 2 RY 4

RESULT 10
US-05-771-192-5
; Sequence 5, Application US/09771192
; Patent No. US20020049152A1
; GENERAL INFORMATION:
; APPLICANT: diferega, Gere
; APPLICANT: diferega, Gere
; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
; FILE REFERENCE: 59-1041
; CURRENT APPLICATION NUMBER: US/09/771.192
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 5
; SEQ ID NO 5
; FEATURE:
; ORGANISM: Artificial Sequence
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:AI1 (2-7)
US-05-771-192-5

Query Match
Best Local Similarity 75.0%; Score 15; DB 10; Length 6;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RY 4
DB 1 RY 3

RESULT 11
US-05-771-192-8
; Sequence 8, Application US/09771192
; Patent No. US20020049152A1
; GENERAL INFORMATION:
; APPLICANT: diferega, Gere
; APPLICANT: diferega, Gere

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; TITLE OF INVENTION: Methods for Inhibiting Smooth Muscle Cell Proliferation
 ; FILE REFERENCE: 99-1043-A
 ; CURRENT APPLICATION NUMBER: US/09/771,192
 ; INVENTOR: KATHLEEN E. ROGERS
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)
 US-09-771-192-8

Query Match 75.0%; Score 15; DB 10; Length 6;
 Best Local Similarity 66.7%; Pred. No. 8,8e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 RY 4

DB 2 RY 4

RESULT 10
 US-09-837-697A-5
 ; Sequence 5, Application US/09837697A
 ; Patent No. US20020146823A1
 ; INVENTOR: KATHLEEN E. ROGERS
 ; APPLICANT: University of Southern California
 ; ADDRESS: 10800 Wilshire Blvd., Suite 1000, Los Angeles, CA 90024
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90024-1000
 ; PHONE: (213) 810-7093
 ; FAX: (213) 810-7093
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PatentIn Ver. 2.0
 ; CURRENT APPLICATION DATA: Version #1.30
 ; APPLICATION NUMBER: US/09/837,697A
 ; CURRENT FILING DATE: 2002-02-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; OTHER INFORMATION: AII(1-7)
 US-09-837-697A-5

Query Match 75.0%; Score 15; DB 10; Length 6;
 Best Local Similarity 66.7%; Pred. No. 8,8e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 RY 4

DB 1 RY 3

RESULT 13
 US-09-837-697A-8
 ; Sequence 8, Application US/09837697A
 ; Patent No. US20020146823A1
 ; INVENTOR: KATHLEEN E. ROGERS
 ; APPLICANT: University of Southern California
 ; ADDRESS: 10800 Wilshire Blvd., Suite 1000, Los Angeles, CA 90024
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90024-1000
 ; PHONE: (213) 810-7093
 ; FAX: (213) 810-7093
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PatentIn Ver. 2.0
 ; CURRENT APPLICATION DATA: Version #1.30
 ; APPLICATION NUMBER: US/09/837,697A
 ; CURRENT FILING DATE: 2002-02-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; OTHER INFORMATION: AII(1-7)
 US-09-837-697A-8

; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: AII(1-6)
 US-09-837-697A-8
 Query Match 75.0%; Score 15; DB 10; Length 6;
 Best Local Similarity 66.7%; Pred. No. 8,8e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 RY 4

DB 2 RY 4

RESULT 14
 US-08-484-409-31
 ; Sequence 31, Application US/08484409
 ; Patent No. US20020076412A1
 ; INVENTOR: STELLAMAN, LAWRENCE
 ; APPLICANT: STELLAMAN, LAWRENCE
 ; ADDRESS: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10104-7093
 ; PHONE: (212) 850-6000
 ; FAX: (212) 850-6000
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA: Version #1.30
 ; APPLICATION NUMBER: US/08/484,409
 ; CURRENT FILING DATE: 2000-03-29
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; REFERENCE/DOCCT NUMBER: 690068.409C1
 ; REGISTRATION NUMBER: 31,392
 ; TELEPHONE: (206) 622-4300
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR PUBLICATION: 31:
 ; SEQ ID NO 31
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-484-409-31

Query Match 65.0%; Score 13; DB 8; Length 4;
 Best Local Similarity 66.7%; Pred. No. 8,8e+04;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 RY 4

DB 1 RY 3

RESULT 15
 US-08-484-409-31
 ; Sequence 10, Application US/09010714
 ; Patent No. US20020012942A1
 ; INVENTOR: MCCARTHY, JAMES B.
 ; APPLICANT: MCCARTHY, JAMES B.
 ; ADDRESS: 10000 Wilshire Blvd., Suite 1000, Los Angeles, CA 90024
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90024-1000
 ; PHONE: (213) 810-7093
 ; FAX: (213) 810-7093
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA: Version #1.30
 ; APPLICATION NUMBER: US/08/484,409
 ; CURRENT FILING DATE: 2000-03-29
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; REFERENCE/DOCCT NUMBER: 690068.409C1
 ; REGISTRATION NUMBER: 31,392
 ; TELEPHONE: (206) 622-4300
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR PUBLICATION: 31:
 ; SEQ ID NO 31
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 US-08-484-409-31


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; FILE REFERENCE: 600.33ZUS01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT PRIORITY NUMBER: 09-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SOURCE: GenBank
; LENGTH: 10
; LATCH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-14-10
Query Match      65.0%; Score 13; Db 10; Length 4;
Query Seq Similarity: 65.0%; Percent Ident: 65.0%;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q# 1 NRI 3
Db 2 NRI 4
Search completed: December 12, 2002, 15:21:21
Job time : 5.2 secs
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GenScope version 5.1.3
Copyright (C) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:58 : Search time 8.8 seconds

(without alignments)
43.697 Million cell updates/sec

Title: US-09-600-432-26

Perfect score: 20

Sequence: 1 ARY 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 43 Summaries

Database: PIR-73*

1: PIR1*

2: PIR2*

3: PIR3*

4: PIR4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
2	13	55.0	4	S62883	seminal plasma pro
2	11	55.0	4	PT0721	T-cell receptor be
3	11	55.0	6	S62883	phytohemagglutinin
4	11	55.0	6	S62883	lysozyme
5	10	50.0	6	249421	laminin B1 - waste
6	9	45.0	4	216883	protamine pI - oca
7	9	45.0	4	216883	protamine pI - oca
8	9	45.0	4	216883	protamine pI - sav
9	9	45.0	5	216702	phosphatase - citrobac
10	9	45.0	5	216702	phosphatase - citrobac
11	9	45.0	5	216702	ribosomal protein
12	9	45.0	5	216702	ribosomal protein
13	9	45.0	5	216702	ribosomal protein
14	9	45.0	6	216702	protamine pI - vor
15	9	45.0	6	PT0568	T-cell receptor be
16	9	45.0	6	PT0568	T-cell receptor be
17	7	35.0	3	A43391	phosphatase - citrobac
18	7	35.0	3	S68328	blood cell protein
19	7	35.0	4	A43039	lysine-melanocort
20	7	35.0	4	A43039	globulin IV alpha
21	7	35.0	4	S04478	Ig heavy chain CHD
22	7	35.0	4	PT0240	Ig heavy chain CHD
23	7	35.0	4	PT0240	Ig heavy chain CHD
24	7	35.0	4	PT0697	T-cell receptor be
25	7	35.0	4	PT0697	T-cell receptor be
26	7	35.0	5	1 H0804	protocollin - Americ
27	7	35.0	5	216469	major protein anti
28	7	35.0	5	216469	major protein anti
29	7	35.0	5	216469	R-phycocyanin ga

30	7	35.0	2	S62883	photoreceptor I 10.4
31	7	35.0	2	B01445	Leu-enkephalin - b
32	7	35.0	2	A61445	Met-enkephalin - b
33	7	35.0	2	S62883	proctolin - Americ
34	7	35.0	2	S62883	proctolin - Americ
35	7	35.0	2	PT0278	Ig heavy chain CHD
36	7	35.0	2	S68328	blood cell protein
37	7	35.0	2	S68328	blood cell protein
38	7	35.0	2	A61445	amelinin - rat
39	7	35.0	2	S11556	hydrogenase-like re
40	7	35.0	2	S11556	hydrogenase-like re
41	7	35.0	2	B33532	Ig mu chain D regi
42	7	35.0	2	F41546	T-cell receptor ga
43	7	35.0	2	F41546	T-cell receptor ga
44	7	35.0	2	P40346	carbon monoxide de
45	6	30.0	4	I40804	endoglucanase P -

ALIGNMENTS

RESULT 1
S62883 plasma protein II - oca (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 28-Oct-1996 Sequence_Revision 13-Mar-1997 Text_Change 17-Mar-1999
C:Accession: S62883
PDB Lett. 362, 15-17, 1996
PDB Lett. 362, 15-17, 1996
A:Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal p
A:Accession: S62883
A:Keywords: glycoprotein; seminal plasma protein I and seminal plasma protein II
A:Molecule type: protein
A:Complex heterodimer; heterodimer; semen
Query Match: 65.0%; Score 13; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match: 65.0%; Score 13; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ARI 3
DB 1 ARI 3

RESULT 2
PT0721 T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 Sequence_Revision 17-Jul-1992 Text_Change 30-May-1997
C:Accession: PT0721
R:Feeney, A. J. 74, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: P05099; MID:51277601; PMID:1711558
A:Accession: PT0721
A:Keywords: T-cell receptor
A:Molecule type: DNA
A:Complex heterodimer; heterodimer; semen
A:Experimental source: newborn thymus, strain BALB/c
Query Match: 55.0%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match: 55.0%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 ARI 3
DB 1 ARI 3

RESULT 3

A:Reference number: 137013; MID:94040810; PMID:8224908
 A:Accession: 137027
 A>Status: Preliminary; translated from CH/PMR/DOB7
 A:Species: Mus musculus (house mouse)
 A:Residues: 1-6 <RES>
 A:Cross-references: EMBL:212145; NID:g22910; PIDN:CM78129; 1: PID:g579612
 Query Match 45.0%; Score 9; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AR 2
 Db 2 AR 3
 RESIDUE 15
 T-cell receptor beta chain V-D-J region (141-1C) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Accession: P0568
 C:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 K:Feeney, A.J.; J. Biol. Chem. 266: 115-124, 1991.
 A:Reference number: P0568; MID:9127760; PMID:1711558
 A:Accession: P0568
 A:Status: Preliminary; translated from CH/PMR/DOB7
 A:Species: Mus musculus (house mouse)
 A:Residues: 1-6 <RES>
 A:Molecule type: mRNA
 A:Residues: 1-6 <RES>
 A:Keywords: T-cell receptor
 Query Match 45.0%; Score 9; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AR 2
 Db 5 AR 6
 Search completed: December 12, 2002, 15:20:08
 Job time : 8.8 secs

OC Eukaryota; Metazoa; Chordata; Grenata; Vertebrata; Euteleostomi;
 RA Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Saitus.
 RN [1] _taxid=10116;

RP SEQUENCE FROM N.A.

RS MEDLINE=1262759; PubMed=1840466;

RA Seto H., Aono S., Kashiwata S., Kawai O.;

RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 blood of a patient with Gilbert's syndrome."

RL Blood. Biophys. Res. Commun. 177:1161-1164(1991).

CC -/- FUNCTION: UDPRT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 EXCRETION OF BILIRUBIN AND OF POTENTIALLY TOXIC XENOBIOTICS AND
 ENDOGENOUS COMPOUNDS.

CC -/- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 + GLUCURONIC ACID.

CC -/- SUBCELLULAR LOCATION: ER.

CC ENBL; S3836; AAB19259.1; .

DR Transferase; glycosyltransferase; Microsome; Multigene family.
 FT NONTER 4 4

SS SEQUENCE 4 AA: 473 MW: 63373242000000 CRC64;

Query Match 15.0%; Score 3; DB 11; Length 4;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 I 3

DB 2 V 2

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Search completed: December 12, 2002, 15:18:46

Job time : 17 secs

OY 2 B 2

DB 2 K 2

Query Match 10.0%; Score 2; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE 5 AA: 623 MW: 6803AAA315F00000 CRC64;

Query Match 10.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 6.7e+05;

GenCorp version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:09:28 Search time 37 seconds

Title: US-09-600-432-39

Perfect score: 25

Sequence: 1 PRRT 5

Scoring table: BL0SGM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 13325020 residues

Total number of hits satisfying chosen parameters: 4205

Minimum db seq length: 0

Maximum db seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 43 summaries

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22: /SID52/sgcdgata/geneexp-emb/AA2001.DAT.*
23: /SID52/sgcdgata/geneexp-emb/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	25	100.0	5	18	AA1984
2	25	100.0	5	20	AA128446
3	25	100.0	5	21	AA15966
4	25	100.0	5	21	AA15966
5	25	100.0	6	21	AA191965
6	18	72.0	5	19	AA121660
7	18	72.0	5	19	AA121660
8	18	72.0	5	20	AA128412
9	18	72.0	5	21	AA191967
10	18	72.0	5	23	AA124333

11	17	68.0	5	5	AA190195
12	17	68.0	5	5	AA190195
13	17	68.0	5	22	AA184782
14	17	68.0	5	22	AA184782
15	17	68.0	5	22	AA184782
16	17	68.0	5	22	AA184782
17	17	68.0	5	22	AA184782
18	17	68.0	5	22	AA184782
19	17	68.0	5	22	AA184782
20	17	68.0	5	22	AA184782
21	17	68.0	5	22	AA184782
22	17	68.0	5	22	AA184782
23	17	68.0	5	22	AA184782
24	17	68.0	5	22	AA184782
25	17	68.0	5	22	AA184782
26	17	68.0	5	22	AA184782
27	17	68.0	5	22	AA184782
28	17	68.0	5	22	AA184782
29	16	64.0	4	20	AA124512
30	16	64.0	4	20	AA124512
31	16	64.0	4	20	AA124512
32	16	64.0	4	20	AA124512
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34	16	64.0	4	20	AA124512
35	16	64.0	4	20	AA124512
36	16	64.0	4	20	AA124512
37	16	64.0	4	20	AA124512
38	16	64.0	4	20	AA124512
39	16	64.0	4	20	AA124512
40	16	64.0	4	20	AA124512
41	16	64.0	4	20	AA124512
42	16	64.0	4	20	AA124512
43	16	64.0	4	20	AA124512
44	16	64.0	4	20	AA124512
45	16	64.0	4	20	AA124512

ALIGNMENTS

RESULT 1
ID AA19842 standard; Peptide: 5 AA.
AC AA19842
XX 26-JAN-1998 (first entry)
DE Chimeric adenovirus coat protein heparin binding motif.
KW Adenovirus; vector; coat protein; gene therapy; gene transfer;
human; cancer; autoimmune disease; heart disease; infection;
heparin.
GS Synthetic.
XX K09720051-A2.
XX K09720051-A2.
PD 27-NOV-1996; 96NC-U019150.
PR 21-AUG-1996; 96US-U01124.
PR 28-NOV-1995; 96US-U05368.
PR 21-AUG-1996; 96US-U070084.
XX (GENV-) GENVEC INC.
PI Brough DR, Kovsed I, Wickham TJ;
DR NPI: 1997-310606/28.
XX Adenoviral vectors containing chimeric coat protein - bind and enter

Sequence of oligop.
Human saliva pep-1
T cell surface rec
Human saliva pep-1
DMM-1 C-terminal
Peptide derivative
Neutrophil activat
Fibronectin pepid
Human saliva pep-1
Human saliva pep-1
DMM-1 C-terminal
DMM-1 C-terminal
Extra cellular mat
Recombinant RSV ge
Human 196 mutant #
Human 196 peptide
Thrombin inhibitor
Sequence of fragile
Human saliva pep-1
Vasopressin frame
C-terminal of GROW
Thrombospondin
Thrombospondin
Lipolytic enzyme o
Interleukin-6 anta
Anticoagulant (15)
Selective factor 1
Human saliva pep-1
Selective factor 1
Human saliva pep-1

CC capacity to facilitate transport of an effector across a biological
 CC membrane. Sequences of the invention are useful for translocating an
 CC effector into the cytoplasm and nucleus of a eukaryotic cell preferably
 CC for the purpose of translocating an effector into the nucleus of a
 CC concentration of an effector within a eukaryotic cell, preferably human
 CC cell. Transporter peptides of the invention are useful for transporting
 CC an effector across a biological membrane for the purpose of translocating
 CC an effector into the nucleus of a eukaryotic cell, preferably human
 CC and for increasing the biological activity of the effector to which
 CC it is coupled. Pharmaceutical compositions comprising the transporter
 CC peptide of the invention are useful for the treatment of cancer, AIDS,
 CC cancer, diabetes, respiratory ailments, neurodegenerative disorders,
 CC cardioplegic and viral infections. The present sequence is a transporter
 CC peptide of the invention. This peptide can be translocated across a
 CC membrane of lung cells.

XX Sequence 5 AA;
 XX Query Watch
 XX Best Local Similarity 72.0%; Score 18; DB 23; Length 5;
 XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRAR 4
 DB 1 PRAR 4

RESULT 11
 AAF50198

ID AAF50198 standard; peptide; 5 AA.

AC AAF50198;

XX 17-OCT-1991 (first entry)

XX Sequence of oligopeptide 1 specific to the beta-subunit of human

XX chorionic gonadotropin (hCG).

XX Contraception; assay; pregnancy test; luteinising hormone;

XX human chorionic gonadotropin.

XX Homo sapiens.

XX EP142387-A.

XX 22-MAY-1985.

XX 23-AUG-1984; 84EP-040710.

XX 26-AUG-1983; 83EP-040714.

XX 23-AUG-1984; 84EP-040710.

XX (ANDA-) ANDA BIOLOGICALS.

XX Wasa RP.

XX WPI; 1985-124152/21.

XX Prep. of anti-hCG and anti-LH vaccines - by use of

XX oligo-peptide(s) specific to beta-sub-unit of LH and hCG

XX Claim 1, Page 17; 22pp; English.

XX Oligopeptides AAF50198-EP0205 - specific to the beta-subunit of LH and

XX for the preparation of anti-hCG and anti-LH vaccines. The vaccines

XX are characterised in that these oligopeptides are complexed upon

XX their own beta-subunit of hCG and LH or upon oligopeptides containing

XX cysteine whose AA chain is common to LH and hCG, namely the peptides

XX an AA chain of 10 amino acids, and the oligopeptides

XX administered by injection in vaccines to cause prodn. of

XX antibodies so that a contraceptive effect is achieved; and the

CC antibodies are also useful in assays for hCG and LH in body fluids.

XX Sequence 5 AA;
 XX Query Watch
 XX Best Local Similarity 68.0%; Score 17; DB 6; Length 5;
 XX Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
 DB 1 PRAR 4

RESULT 12
 AAF74622

ID AAF74622 standard; peptide; 5 AA.

AC AAF74622;

XX 21-OCT-1998 (first entry)

XX Analogue of chymotrypsin-cleaved supAR peptide 9.

XX Homo; urokinase receptor; uPAR; soluble uPAR; supAR; chymotrypsin;

XX cleavage; cancer; autoimmune disease; inflammatory disorder;

XX wound healing; antigen; vaccination; HIV.

XX Homo sapiens.

XX WO942733-A1.

XX 01-OCT-1998.

XX 18-MAR-1998; 98NO-EP01547.

XX 20-MAR-1997; 97US-0041112.

XX (SNAR-) FOND CENT SAN RAFFAELLE DEL MONTE TABOR.

XX (UTM-) UNIV MILAN STUDI.

XX Blasi F, Paroli F, Nicolai S, Resnati N;

XX WPI; 1998-531945/5.

XX New soluble urokinase receptor products obtained by chymotrypsin

XX cleavage - useful for, e.g. treating cancers, autoimmune diseases

XX and inflammatory disorders or for stimulating wound healing

XX Disclosure; Page 13; 59pp; English.

XX This is the nucleotide sequence of a functional analogue of the

XX chymotrypsin-cleaved human soluble urokinase receptor (supAR)

XX peptide used in the method of the invention. In this process supAR

XX is cleaved by chymotrypsin to produce a soluble urokinase receptor,

XX autoimmune disease, inflammatory disorders, supAR peptide or its

XX functional peptide may be used for stimulating or increasing wound

XX healing. The soluble urokinase receptor or its functional peptide

XX sequence SSSRV or its functional analogue may be used for stimulating

XX or increasing, e.g. the chemotactic activity of a cell, a local

XX inflammatory response and anti-tumour activity in an animal model

XX patient, who is immunodeficient. These products may also be used for

XX increasing the immunodeficiency of antigens in vaccination, e.g. against

XX viral infections such as HIV infection.

XX Sequence 5 AA;
 XX Query Watch
 XX Best Local Similarity 75.0%; Score 17; DB 19; Length 5;
 XX Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRAR 4
 DB 1 PRAR 4

DB 1 PGRH 4

RESULT 13

AA484782

ID AA484782 standard; peptide; 5 AA.

AC AA484782;

XX 09-MAR-2001 (first entry)

XX Human saliva PRP-1 fragment (residues 104-108), SEQ ID NO:12.

DE Human: PRP-1; proline-rich protein; saliva; dental caries;

DE chromosome 12p13.2; arginine catabolism; ammonia production;

KW pH increase; oral bacterium; caries prevention.

OS Homo sapiens.

XX W020006980-A1.

XX 23-NOV-2000.

PD 11-MAY-2000; 2000NC-S800930.

XX 17-MAY-1999; 95SF-0001773.

PR (STRO// STROMBERG N.

PA (JOBA// JOHANSSON J.

XX Stromberg N, Johansson J;

XX WPI: 2001-001223/04.

XX New oligopeptides comprising 2 arginine residues from degradation of

PT proline-rich proteins, useful for preventing dental caries -

PS Claim 4; Page 24; 3pp; English.

XX This invention relates to human PRP-1-derived oligopeptides (AA484771-
 AA484783) which, at a concentration of 10⁻⁶ M, protect against dental caries. PRPs (proline-rich proteins) are salivary proteins encoded by six clustered genes on chromosome 12p13.2 and are degraded by *Actinomyces* and *Streptococcus* species to small peptide fragments. These are metabolized by oral bacteria for ammonia production. The peptide fragments generate ammonia via the catabolism of arginine. The peptide fragments, which are arginine-rich, can also be converted to ammonia by these bacteria. The ammonia thus formed raises the pH at the dental surface, thereby inhibiting the growth of cariogenic bacteria. AA484771-AA484783 represent the PRP-1-derived oligopeptides of the invention.

XX Sequence 5 AA:

Query Match 88.0%; Score 17; DB 22; Length 5;
 Identical Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PGRH 4

DB 2 PGRH 5

RESULT 14

AA485601

ID AA485601 standard; Peptide; 5 AA.

AC AA485601;

XX 07-MAR-2001 (first entry)

XX T cell surface receptor PDZ domain sequence #72.

DE T cell surface receptor PDZ domain sequence #72.

XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
 KW allergy; asthma; multiple sclerosis; cancer; infection.

OS Synthetic.

XX W020006986-A2.

XX 23-NOV-2000.

PD 12-MAY-2000; 2000NC-US13161.

XX 14-MAY-1999; 950S-0134114.

PR 14-MAY-1999; 950S-0134114.

FR 14-MAY-1999; 950S-0134118.

PR 21-OCT-1999; 950S-0160860.

PR 13-OCT-1999; 950S-0174648.

PR 13-OCT-1999; 950S-0174648.

PR 14-JAN-2000; 2000NS-0176195.

PR 14-FEB-2000; 2000NS-0182296.

PR 11-APR-2000; 2000NS-0186527.

XX (AA485-1) ABBOR VITA CORP.

XX Lu PS;

PT Mediating a biological function of an endothelial cell or infectious diseases, by administering an antagonist that inhibits binding between a PDZ protein and a PL protein -

PS Disclosure; Page 87-94; 14pp; English.

XX The present invention relates to a new method for modulating a cell's biological function. The method involves introducing into a cell, an antagonist that inhibits binding between a PDZ protein and a PL protein. The inhibitor is used to treat infectious diseases, such as autoimmune diseases, e.g., autoimmune disease. It may also be used to prevent or treat diseases, e.g., autoimmune disease, inflammatory bowel diseases, ulcerative colitis, inflammation, allergy, inflammatory bowel diseases, alternative diseases (e.g., rheumatoid arthritis, multiple sclerosis, autoimmune diseases), insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis, osteoporosis, multiple sclerosis, multiple sclerosis, multiple sclerosis, infectious diseases, ischemia, vasculitis and Crohn's disease.

XX Sequence 5 AA:

Query Match 68.0%; Score 17; DB 22; Length 5;
 Identical Similarity 40.0%; Pred. No. 7.8e+05;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 PGRH 5

DB 1 PGRH 5

RESULT 15

AA4857448

ID AA4857448 standard; Peptide; 5 AA.

AC AA4857448;

XX 12-MAR-2001 (first entry)

XX DNM-1 C-terminal core sequence #2.

DE Endothelial cell; hematopoietic cell; PDZ domain protein;
 KW PL domain protein; leukocyte activation; T cell surface receptor;


```

1 APPLICANT: Allen, Janice B.
2 APPLICANT: Billups, Kevin L.
3 APPLICANT: Everett, Jeffrey E.
4 APPLICANT: Farnsworth, Robert L.
5 TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
6 NUMBER OF SEQUENCES: 15
7 CROSS-REFERENCE TO PRIOR APPLICATION: US-09/008,308
8 ADDRESS: Macchabert & Gould
9 STREET: 30 South 7th Street, 3100 No. 5840691west Center
10 CITY: Minneapolis
11 STATE: Minnesota
12 COUNTRY: USA
13 ZIP: 55402
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC DOS/MS-DOS
16 SOFTWARE: Patent Release 11.0, Version 11.30
17 MEDIUM TYPE: Floppy disk
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/480,133A
20 CLASSIFICATION: C12N-1/35
21 PRIOR APPLICATION DATA: US 08/139,903
22 FILING DATE: 21-OCT-1993
23 PRIORITY DATE: 07/09/90,296
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Carter, Charles G.
26 TELEPHONE: 612-332-6030
27 TELEFAX: 612-332-6031
28 TELECOMMUNICATION INFORMATION:
29 REFERENCE/DOCKET NUMBER: 600-108U501
30 INFORMATION FOR SEQ ID NO: 15:
31 SOURCE CHARACTERISTICS:
32 TYPE: amino acid
33 STRANDNESS: linear
34 US-08-480-133A-15
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36 Query Match 72.0% Score 18; DB 2; Length 4;
37 Best Local Similarity 100.0% Pred. No. 1.9e+05;
38 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
39
40 Oy 2 RARI 5
41 Db 1 RARI 4
42
43 RESULT 3
44 US-09-008-308-30
45 SEQ ID NO 30: Application US/09008308
46 Patent No. 6080575
47 GENERAL INFORMATION:
48 APPLICANT: Masahito, Hans II.
49 APPLICANT: Mueller, Rolf
50 APPLICANT: Sedlacek, Hans-Harald
51 TITLE OF INVENTION: CONSTRUCT FOR EXPRESSING
52 ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES; AND
53 OTHER INFORMATION: PREPARATION AND USE
54 CROSS-REFERENCE TO PRIOR APPLICATION: US-08-139,903
55 ADDRESS: Poley & Lardner
56 STREET: 3000 K Street, N.W., Suite 500
57 CITY: Washington
58 STATE: D.C.
59 COUNTRY: USA
60 MEDIUM TYPE: Floppy disk

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1 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC DOS/MS-DOS
3 SOFTWARE: Patent Release 11.0, Version 11.30
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: US/09/008,308
6 CLASSIFICATION: C12N-1/35
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: US-197 01 141.1
9 ATTORNEY/AGENT INFORMATION:
10 NAME: Sandercock, Colin G.
11 TELEPHONE: 612-332-6258
12 TELECOMMUNICATION INFORMATION:
13 REFERENCE/DOCKET NUMBER: 026083/0189
14 TELEPHONE: 612-332-6300
15 TELEFAX: 612-332-6300
16 INFORMATION FOR SEQ ID NO: 30:
17 SOURCE CHARACTERISTICS:
18 TYPE: amino acid
19 STRANDNESS: linear
20 TOPOLOGY: linear
21 MOLECULE TYPE: peptide
22 FRAGMENT TYPE: internal
23 US-09-600-308-30
24
25 Query Match 72.0% Score 18; DB 3; Length 4;
26 Best Local Similarity 100.0% Pred. No. 1.9e+05;
27 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
28
29 Oy 2 RARI 5
30 Db 1 RARI 4
31
32 RESULT 4
33 US-09-381-2448-13
34 SEQ ID NO 13: Application US/093812448
35 Patent No. 6463170
36 GENERAL INFORMATION:
37 APPLICANT: ELASI, FRANCESCO
38 APPLICANT: KIMURA, Masahito
39 APPLICANT: RESNATI, Massimo
40 APPLICANT: NICOLAI, Sidenius
41 TITLE OF INVENTION: Immunomodulating Peptide
42 OTHER INFORMATION:
43 FILE REFERENCE: 0471-0143p
44 CURRENT APPLICATION NUMBER: US/09/381,2448
45 CROSS-REFERENCE TO PRIOR APPLICATION: US-09-381,2448
46 PRIOR APPLICATION NUMBER: PCT/JP95/01547
47 PRIOR FILING DATE: 1998-03-18
48 NUMBER OF SEQ ID NOS: 28
49 SEQ ID NO 13:
50 LENGTH: 5
51 ORGANISM: Homo sapiens
52 ORGANISM: Artificial Sequence
53 FEATURE:
54 OTHER INFORMATION: Description of Artificial Sequence: synthetic
55 OTHER INFORMATION: peptide analogue of the human UPAR
56 US-09-381-2448-13
57
58 Query Match 72.0% Score 18; DB 4; Length 5;
59 Best Local Similarity 75.0% Pred. No. 1.9e+05;
60 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
61
62 Oy 1 PRAR 4
63 Db 1 PRAR 4
64
65 RESULT 5

```

```

US-08-375-879-4
: Application US/08375879
: Patent No. 5514608
: GENERAL INFORMATION:
: APPLICANT: Schering, Viktor
: INVENTOR: Schering, Michael
: APPLICANT: Schering, Michael
: TITLE OF INVENTION: Apparatus and Method for Multiple
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS: Esbende
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: SOFTWARE: Patented software, US/88-808
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/007/375,879
: APPLICATION DATE: JAN-1995
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: 18872
: REFERENCE/DOCKET NUMBER: 7156-068
: TELEPHONE: (212) 791-9090
: TELEFAX: (212) 869-1864
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-375-879-4
:
: Query Match 68.0%; Score 17; DB 1; Length 5;
: Best Local Similarity 75.0%; Pred. No. 1.9e+05;
: Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
:
: QY 1 PRAR 4
: DB 2 PRGR 5
:
: RESULT 5
: US-09-515-517A-42
: Sequence 42, Application US/0912517A
: Patent No. 6087136
: GENERAL INFORMATION:
: APPLICANT: Condon, Ronald
: INVENTOR: Edwards, Philip Neil
: TITLE OF INVENTION: Peptide Derivatives
: NUMBER OF SEQUENCES: 62
: CORRESPONDENCE ADDRESS: Flagg, Ernst & Kurz, P.C.
: STREET: 555 Thirteenth St., N.W., Suite 701 East
: CITY: Denver
: STATE: CO
: COUNTRY: U.S.A.
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: APPLICATION DATE: JAN-1995
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/125-517A
: APPLICATION DATE: JAN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 9603855.9
: FILING DATE: MAR-1995
: PRIORITY DATE: MAR-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 9520819.4
: FILING DATE: MAR-1995
: PRIORITY DATE: MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Ernst, Barbara G.
: REFERENCE/DOCKET NUMBER: 1991-127
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 783-6031
: TELEFAX: 202-783-6031
: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-125-517A-42
:
: Query Match 68.0%; Score 17; DB 3; Length 5;
: Best Local Similarity 75.0%; Pred. No. 1.9e+05;
: Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
:
: QY 2 RARI 5
: DB 2 RARI 5
:
: RESULT 7
: US-09-284-625-6
: Sequence 6, Application US/09284625
: Patent No. 6067614
: GENERAL INFORMATION:
: APPLICANT: Lake, Richard William
: TITLE OF INVENTION: Peptide Analogues Containing a 7-membered Lactam Ring
: FILE REFERENCE: 1991-169
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/284,625
: CURRENT FILING DATE: 1995-04-16
: PRIOR APPLICATION NUMBER: PCT/GB97/02837
: PRIORITY DATE: DEC-1996
: PRIOR APPLICATION NUMBER: GB 96218367
: PRIOR FILING DATE: 1996-10-19
: NUMBER OF SEQ ID NOS: 30
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQ ID NO 6
: ORGANISM: Homo sapiens
US-09-284-625-6
:
: Query Match 68.0%; Score 17; DB 4; Length 5;
: Best Local Similarity 75.0%; Pred. No. 1.9e+05;
: Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
:
: QY 2 RARI 5
: DB 2 RARI 5
:
: RESULT 8
: US-09-381-244B-15
: Sequence 15, Application US/09381244B
: Patent No. 6462170

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Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PART 5
DB 3 PART 6

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RESULT 11
; Sequence 5, Application US/08240514
; Patent No. 5670147
; GENERAL INFORMATION: T. Vester
; TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS: Peetitia
; ADDRESS: Kipling Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: Washington
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PseEdit, Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/240,514
; APPLICATION NUMBER: 5670147
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 73921/102/CLIN
; TELEPHONE: (202)692-5198
; TELEFAX: (202)692-5199
; INFORMATION: 90436
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 4 amino acids
; STRANDNESS: single
; TOPOLOGY: linear
; US-08-240-514-5

Query Match
Best Local Similarity 64.0%; Score 16; DB 1; Length 4;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PART 4
DB 1 PART 4

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PseEdit, Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/612,302A
; APPLICATION NUMBER: US/08/612,302A
; CLASSIFICATION: 7
; ATTORNEY/AGENT INFORMATION:
; NAME: Amsel, Viviana
; ADDRESS: 30, 930
; STREET: 10101457000
; CITY: Washington
; STATE: n.a.
; COUNTRY: n.a.
; ZIP: (610) 407-0701
; TELEFAX: (610) 407-0701
; REFERENCE/DOCKET NUMBER: AMRA-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 407-0700
; TELEFAX: (610) 407-0701
; INFORMATION FOR SEQ ID NO: 5:
; LENGTH: 4 amino acids
; STRANDNESS: single
; TOPOLOGY: n.a.
; US-08-612-302A-5

Query Match
Best Local Similarity 75.0%; Score 16; DB 2; Length 4;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PART 4
DB 1 PART 4

```

```

RESULT 13
; Sequence 421, Application US/08637759B
; Patent No. 5876911
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; CORRESPONDENCE ADDRESS:
; ADDRESS: Patrea L. Pabst
; STREET: 2900 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; ZIP: 30309-3430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PseEdit, Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/637,759B
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PC/GB95/02875
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; ADDRESS: 131, 284
; STREET: One Westlakes Drive N
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; TELEFAX: (484) 873-8795
; INFORMATION FOR SEQ ID NO: 421:
; LENGTH: 1 amino acid
; TYPE: amino acid

```



```

; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-09-577-531-30

```

```

Query Match
Best Local Similarity 72.0%; Score 16; Db 10; Length 5;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 1 PRA 4
```

```
DB 1 PRA 4
```

```

RESULT 3
US-10-024-918-7
; Sequence 7, Application US/1004918
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey
; APPLICANT: Hubbell, Jeffrey
; APPLICANT: zisch, Andrew
; APPLICANT: Hall, Heike
; TITLE OF INVENTION: SYSTEM-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE ENGINEERING
; CURRENT FILING DATE: 2001-12-18
; PRIOR FILING DATE: 2001-12-18
; CURRENT APPLICATION NUMBER: US/10/024-918
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; SEQ ID NO 8
; TYPE: PRT
; FEATURE:
; ORGANISM: artificial sequence
; ORGANISM: heparin-binding sequence from fibronectin
US-10-024-918-7

```

```

Query Match
Best Local Similarity 75.0%; Score 17; Db 9; Length 6;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 2 PRA 5
```

```
DB 3 PRA 6
```

```

RESULT 4
US-09-460-20
; Sequence 20, Application US/09887469
; Patent No. US2002014613A1
; GENERAL INFORMATION:
; APPLICANT: Christine D.
; APPLICANT: Collins, Peter L.
; APPLICANT: Murphy, Brian R.
; APPLICANT: Whithead, Stephen S.
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES EXPRESSING
; TITLE OF INVENTION: RESPIRATORY ANTIGENS FROM PROCTOR PROXIMAL GLIROS
; FILE REFERENCE: 15280-424-US
; CURRENT FILING DATE: US/09/887,469
; PRIOR FILING DATE: 15280-424-US
; CURRENT APPLICATION NUMBER: US/09/887,469
; PRIOR APPLICATION NUMBER: US/01/001,708
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20

```

```

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: Respiratory Syncytial Virus
US-09-487-469-20

```

```

Query Match
Best Local Similarity 68.0%; Score 17; Db 10; Length 6;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 2 PRA 5
```

```
DB 1 PRA 4
```

```

RESULT 5
US-09-402-077-59
; Sequence 59, Application US/09402077
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2CJUS US/09/402,077
; CURRENT APPLICATION NUMBER: US/09/402,077
; PRIOR APPLICATION NUMBER: US/08/405,617
; PRIOR FILING DATE: 1992-05-15
; PRIOR FILING DATE: 1994-01-26
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR APPLICATION NUMBER: US/07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1991-08-24
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 59
; SEQ ID NO 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-402-077-59

```

```

Query Match
Best Local Similarity 100.0%; Score 16; Db 10; Length 4;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 1 PRA 3
```

```
DB 1 PRA 3
```

```

RESULT 6
US-09-402-096-59
; Sequence 59, Application US/09402096
; Patent No. US2002014613A1
; GENERAL INFORMATION:
; APPLICANT: Jardiou, Paula M.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2CJUS
; CURRENT APPLICATION NUMBER: US/09/402,096
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US/08/405,617
; PRIOR FILING DATE: 1992-05-15
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR APPLICATION NUMBER: US/07/879,495
; PRIOR FILING DATE: 1992-05-07

```


; PRIOR APPLICATION NUMBER: US 07/744,768
 ; PRIOR FILING DATE: 1991-08-14
 ; INVENTOR: SEQ ID NOS: 64
 ; SEQ ID NO 59
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-807-096-59

Query Match 64.0%; Score 16; DB 10; Length 4;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRAI 3
 DB 1 PRA 3

RESULT 7
 ; Sequence 17, Application US/10036418
 ; Patent No. US20020127624A1
 ; INVENTOR: SEQ ID NOS: 64
 ; APPLICANT: Taylor-Fishwick, David
 ; TITLE OF INVENTION: INCAP Displacement Assay
 ; CURRENT APPLICATION NUMBER: US/10/036,418
 ; CURRENT FILING DATE: 2002-01-07
 ; PRIOR FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FASTSQ for Windows Version 4.0
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Cricetus

US-10-036-418-17

Query Match 64.0%; Score 16; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PRAI 5
 DB 2 PSSRI 6

RESULT 8
 ; Sequence 17, Application US/10036418
 ; Patent No. US20020127624A1
 ; INVENTOR: SEQ ID NOS: 64
 ; APPLICANT: Taylor-Fishwick, David
 ; TITLE OF INVENTION: INCAP Displacement Assay
 ; CURRENT APPLICATION NUMBER: US/10/036,418
 ; CURRENT FILING DATE: 2002-01-07
 ; PRIOR FILING DATE: 2002-01-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FASTSQ for Windows Version 4.0
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Cricetus

Query Match 64.0%; Score 16; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 PRAI 5
 DB 1 PSSRI 5

RESULT 9

; Sequence 5, Application US/10066151
 ; Patent No. US2002012300A1
 ; INVENTOR: SEQ ID NOS: 64
 ; APPLICANT: Hogan, Patrick C.
 ; TITLE OF INVENTION: SPECIFIC INHIBITORS OF NFAT ACTIVATION
 ; CURRENT APPLICATION NUMBER: US/09/066,151
 ; CURRENT FILING DATE: 2002-01-21
 ; PRIOR APPLICATION NUMBER: 09/248,620
 ; PRIOR FILING DATE: 1998-02-12
 ; NUMBER OF SEQ ID NOS: 114
 ; SOFTWARE: FASTSQ for Windows Version 4.0
 ; LENGTH: 6
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-066-151-5

Query Match 60.0%; Score 15; DB 12; Length 6;
 Best Local Similarity 60.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 PRAI 5
 DB 1 PHEI 5

RESULT 10
 ; Sequence 5, Application US/09800433
 ; Patent No. US20020106378A1
 ; INVENTOR: SEQ ID NOS: 64
 ; APPLICANT: O'Hanlon, Elliott
 ; TITLE OF INVENTION: Materials and methods for intracellular transport and
 ; FILX REFERENCE: 09800433
 ; CURRENT APPLICATION NUMBER: US/09/800,433
 ; CURRENT FILING DATE: 2000-03-05
 ; PRIOR FILING DATE: 1999-09-13
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patent Ver. 2.0
 ; LENGTH: 5
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

US-09-800-433-5

; OTHER INFORMATION: Description of Artificial Sequence: peptide
 ; Feature:

Query Match 56.0%; Score 14; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRA 4
 DB 3 PRA 5

RESULT 11

```

US-09-800-433-7
: Sequence 7, Application US/09800433
: Patent No. US60378A1
: GENERAL INFORMATION:
: APPLICANT: O'Hare and Elliott
: TITLE OF INVENTION: Materials and methods for intracellular transport and
: delivery of nucleic acids and their uses
: FILE REFERENCE: 49408
: CURRENT APPLICATION NUMBER: US/09/000,433
: PRIORITY FILING DATE: 1998-09-13
: PRIOR APPLICATION NUMBER: 09/395,344
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 7
: LENGTH: 5
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-800-433-7
: TYPE: PPT
: FEATURE: Artificial Sequence
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Peptide
US-09-947-387-47
: Query Match
: Best Local Similarity 56.0%; Score 14; DB 10; Length 5;
: Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PAR 4
Db 3 PAR 5
RESULT 12
US-09-977-431-19
: Sequence 12, Application US/09977831
: Patent No. US6020120100A1
: GENERAL INFORMATION:
: APPLICANT: Swiss Transfer Office University of Lausanne
: APPLICANT: PACIFIC CYCLARIS
: TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
: FILE REFERENCE: 2049-512 Transporter peptides
: CURRENT APPLICATION NUMBER: US/09/977,831
: PRIORITY FILING DATE: 2001-10-15
: PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 9
: LENGTH: 9
: ORGANISM: Artificial Sequence
: TYPE: PPT
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
: OTHER INFORMATION: PEPTIDE
US-09-977-431-19
: Query Match
: Best Local Similarity 56.0%; Score 14; DB 10; Length 5;
: Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PAR 4
Db 3 PAR 5
RESULT 13
US-09-947-387-47
: Sequence 13, Application US/09947387
: Patent No. US60378A1
: GENERAL INFORMATION:
: APPLICANT: Weber, Eckard
: APPLICANT: Kensa John F M,
: APPLICANT: Brown, John A.
: APPLICANT: Zhang, Han-zhong
: TITLE OF INVENTION: Fluorescent or Fluorescent Reporter Mole
: cules and Methods for Screening Assays for Campases and Other Enzymes and the
: Use Thereof
: FILE REFERENCE: 49408
: CURRENT APPLICATION NUMBER: US/09/947,387
: PRIORITY FILING DATE: 2001-09-07
: PRIOR APPLICATION NUMBER: US 60/061,582
: PRIORITY FILING DATE: 1998-03-03
: PRIOR APPLICATION NUMBER: US 60/745,746
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 1
: LENGTH: 5
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: Peptide
US-09-947-387-47
: Query Match
: Best Local Similarity 56.0%; Score 14; DB 10; Length 5;
: Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PAR 5
Db 1 KARY 4
RESULT 14
US-09-823-823-66
: Sequence 14, Application US/09823823
: Patent No. US620020171092A1
: GENERAL INFORMATION:
: APPLICANT: Kensa, Hiroaki
: APPLICANT: Nakamura, Shoko
: APPLICANT: Suzuki, Makoto
: APPLICANT: Kushi, Hiroaki
: TITLE OF INVENTION: METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING
: A GENE AS AN INDICATOR
: CURRENT APPLICATION NUMBER: US/09/823,823
: PRIORITY FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: US 09/208,688
: PRIOR APPLICATION NUMBER: JP 97/34316
: PRIORITY FILING DATE: 1997-12-12
: SOFTWARE: Patentin version 2.0
: SEQ ID NO 66
: LENGTH: 6
: ORGANISM: Artificial Sequence
: TYPE: PPT
: FEATURE:
: OTHER INFORMATION: Synthetically generated protein
US-09-823-823-66
: Query Match
: Best Local Similarity 100.0%; Score 14; DB 9; Length 6;
: Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 PAR 4
Db 3 PAR 5
RESULT 15

```

```

US-09-594-599A-3
; Patent No.: US20020075419A1
; GENERAL INFORMATION:
; INVENTOR: Charles Jeffrey A.
; APPLICANT: Charles Jeffrey A.
; TITLE OF INVENTION: Ligands Added to Adenovirus Fiber
; PRIORITY INFORMATION: US 09/594-599A
; CURRENT APPLICATION NUMBER: US/09/404,599A
; FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 08/719,369
; PRIORITY INFORMATION: With Trimerization
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 3
; (CDS)
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: peptide that can be added to the c-terminus
; OTHER INFORMATION: of the fiber protein without interfering
; OTHER INFORMATION: with trimerization
US-09-594-599A-3
Query Match Score 14; DB 10; Length 6;
Similarity 100.0%; B 86.04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PAR 4
DB 3 PAR 5

```

Search completed: December 12, 2002, 15:21:21
 Job time : 5.25 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:58 ; Search time 11 seconds
(without alignments)
43,697 Million cell updates/sec

Title: us-09-600-432-39

Score: 2.98481

Sequences: 1

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 282224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 316

Minimum DB seq length: 0

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

5: p1r5:*

6: p1r6:*

7: p1r7:*

8: p1r8:*

9: p1r9:*

10: p1r10:*

11: p1r11:*

12: p1r12:*

13: p1r13:*

14: p1r14:*

15: p1r15:*

16: p1r16:*

17: p1r17:*

18: p1r18:*

19: p1r19:*

20: p1r20:*

21: p1r21:*

22: p1r22:*

23: p1r23:*

24: p1r24:*

25: p1r25:*

26: p1r26:*

27: p1r27:*

28: p1r28:*

29: p1r29:*

30: p1r30:*

31: p1r31:*

32: p1r32:*

33: p1r33:*

34: p1r34:*

35: p1r35:*

36: p1r36:*

37: p1r37:*

38: p1r38:*

30 7 28.0 3 492971
31 7 28.0 3 433802
32 7 28.0 3 443391
33 7 28.0 3 453399
34 7 28.0 4 463399
35 7 28.0 4 473399
36 7 28.0 4 483399
37 7 28.0 4 493399
38 7 28.0 4 503399
39 7 28.0 4 513399
40 7 28.0 4 523399
41 7 28.0 4 533399
42 7 28.0 4 543399
43 7 28.0 4 553399
44 7 28.0 4 563399
45 7 28.0 5 2 A66521

ALIGNMENTS

RESULT 1
S62883 Plasma protein II - pig (fragment)
C:Species: Sus scrofa domestica (pig)
C:Date: 28-Oct-1996 sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S62883
C:Keywords: glycoprotein; heterodimer; semen
F885 Lett. 362, 15-17, 1996
Article: Crystallization and preliminary X-ray diffraction analysis of boar seminal p
A:Accession: S62883
A:Keywords: glycoprotein; heterodimer; semen
A:Molecule type: protein
C:Residues: 55 amino acids
C:Length: 55
C:Query Match: 52.0% ; Score 13; DP 2; length 5;
Best Local Similarity 100.0% ; Pred No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match: 52.0% ; Score 13; DP 2; length 5;
Best Local Similarity 100.0% ; Pred No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match: 52.0% ; Score 13; DP 2; length 5;
Best Local Similarity 100.0% ; Pred No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match: 52.0% ; Score 13; DP 2; length 5;
Best Local Similarity 100.0% ; Pred No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match: 52.0% ; Score 13; DP 2; length 5;
Best Local Similarity 100.0% ; Pred No. 2.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	13	52.0	5	2	562883			seminal plasma pro
2	12	48.0	4	2	A02147			phagocytosis-stimu
3	11	48.0	6	2	PF0518			T-phycoerythrin al
4	12	48.0	6	2	PF0518			T-cell receptor be
5	11	44.0	4	2	PF0721			peptidyl-dipeptida
6	10	40.0	6	2	2N4690			Orf 3 rata 5'-regi
7	10	40.0	6	4	515596			prolactin PI - Ora
8	10	40.0	6	4	515596			prolactin PI - Ora
9	9	36.0	4	2	105883			prolactin PI - Ora
10	9	36.0	4	2	184439			prolactin PI - Ora
11	9	36.0	5	2	412225			Copper resistance
12	9	36.0	5	2	412225			Copper resistance
13	9	36.0	5	2	412225			Copper resistance
14	9	36.0	5	2	412225			Copper resistance
15	9	36.0	5	2	412225			Copper resistance
16	9	36.0	5	2	412225			Copper resistance
17	9	36.0	5	2	412225			Copper resistance
18	9	36.0	5	2	412225			Copper resistance
19	9	36.0	5	2	412225			Copper resistance
20	9	36.0	5	2	412225			Copper resistance
21	9	36.0	5	2	412225			Copper resistance
22	9	36.0	5	2	412225			Copper resistance
23	9	36.0	5	2	412225			Copper resistance
24	8	32.0	6	2	PF0518			T-cell receptor be
25	8	32.0	6	2	PF0518			T-cell receptor be
26	8	32.0	6	2	PF0518			T-cell receptor be
27	8	32.0	6	2	PF0518			T-cell receptor be
28	8	32.0	6	2	PF0518			T-cell receptor be
29	8	32.0	6	2	PF0518			T-cell receptor be

Query Match: 52.0% ; Score 13; DP 2; length 4;
Best Local Similarity 100.0% ; Pred No. 2.8e+05; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C:Comment: This sequence is not thought to be translated.

A:Gene: GSN-RADA

A:Cross-references: GSN:120337; OMIM:180240

A:Map position: 17q12-17q12

Query Match 40.0%; Score 10; DB 4; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05; Gaps 0;

Matches 2; Conservative 0; Mismatches 1; Indels 0;

Qy 1 PR 3

Db 3 PR 5

RESULT 9

proteamine p1 - orangutan (fragment)

A:Accession: I61883

C:Date: 06-Sep-1997 sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

C:Species: Pseudomys oranga (Orangutan)

Q:Query: 157-204, 1993

A:Title: Identification of conserved potential regulatory sequences of the proteamine-end

A:Reference number: 137013; PMID:9404810; PMID:8224908

A:Status: Preliminary; translated from GB/DML/DDBJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references: DML:1212146; NID:938156; PID:CMV7130.1; PID:9437972

Query Match 36.0%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 3 AR 4

Db 2 AR 3

RESULT 10

137013

proteamine p1 - Cercopithecus gates (fragment)

C:Species: Cercopithecus

C:Date: 19-Mar-1997 sequence_revision 07-Nov-1997 #text_change 21-Jul-2000

A:Accession: 137013

Q:Query: 157-204, 1993

A:Title: Identification of conserved potential regulatory sequences of the proteamine-end

A:Reference number: 137013; PMID:9404810; PMID:8224908

A:Status: Preliminary; translated from GB/DML/DDBJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references: DML:1212150; NID:922814; PID:CMV7134.1; PID:94377415

Query Match 36.0%; Score 9; DB 3; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 3 AR 4

Db 2 AR 3

RESULT 11

137013

proteamine p1 - savannah baboon (fragment)

C:Species: Papio hamadryas doguera (savannah baboon)

C:Date: 19-Mar-1997 sequence_revision 07-Nov-1997 #text_change 21-Jul-2000

A:Accession: 18439

Q:Query: 157-204, 1993

A:Title: Identification of conserved potential regulatory sequences of the proteamine-end

A:Reference number: 137013; PMID:9404810; PMID:8224908

A:Status: Preliminary; translated from GB/DML/DDBJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Title: Identification of conserved potential regulatory sequences of the proteamine-end

A:Reference number: 137013; PMID:9404810; PMID:8224908

A:Status: Preliminary; translated from GB/DML/DDBJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references: DML:1212147; NID:938134; PID:CMV7133.1; PID:9437949

Query Match 36.0%; Score 9; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 3 AR 4

Db 2 AR 3

RESULT 12

CM1225

resistance protein - Pseudomonas syringae pv. tomato (fragment)

C:Species: Pseudomonas syringae pv. tomato

C:Date: 19-Jun-1992 sequence_revision 18-Jun-1992 #text_change 24-Jun-1993

A:Accession: CM1225

Q:Query: 157-204, 1993

A:Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer

A:Reference number: CM1225; PMID:9202061; PMID:1924351

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-5 <RES>

Query Match 36.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Gaps 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0;

Qy 1 PR 2

Db 2 PR 3

RESULT 13

160702

Glucanase divergens (fragment)

C:Species: Glucanase divergens

C:Date: 16-Aug-1996 sequence_revision 16-Aug-1996 #text_change 16-Aug-1996

A:Accession: 160702

Q:Query: 157-204, 1993

A:Title: Conservation and evolution of the TpaU-dnaG-rpoD macromolecular synthesis (M

A:Reference number: 160702; PMID:9302510; PMID:8316085

A:Status: Preliminary; translated from GB/DML/DDBJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

A:Cross-references: GB:101754; NID:9144439

C:Genetics:

A:Gene: dnaG

Query Match 36.0%; Score 9; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0;

Qy 4 RI 5

Db 4 RI 5

RESULT 14

139584

cellulose synthase protein, cy

C:Species: Neisseria meningitidis (fragment)

C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996

C:Accession: J39964
 C:Entry: F. J. Henkle, T. M. 1992
 A:Title: Characterization of the Bacillus subtilis σ^H regulatory target site.
 A:Reference number: 19963; MID:9301575; PMID:1400226
 A:Accession: J39964
 A:Status: preliminary; translated from GB/DNAL/DDBJ
 A:Molecule type: DNA
 A:Source: *Bacillus subtilis* 168
 A:Cross-references: GB:99041; MID:g13471
 C:Genetics: 1

Query Match 36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Idels 0; Gaps 0;

Qy	3	AR	4
		II	
Db	2	AR	3

RESULT 15

1996a, Protein M; *Sacillus licheniformis* fragment).
Species: *Sacillus licheniformis*.
C Date: 19-Jul-1996 sequence revision 19-Jul-1996 text_change 19-Jul-1996
C Date: 19-Jul-1996 sequence revision 19-Jul-1996 text_change 19-Jul-1996
R Grundy, F.J.; Benklt, T.M.
S accession number: 5781-6702 1992
A Reference number: 19863; MTD:9.901735; MBL:1400226
A Status: preliminary Translated from GB/EMBL/DDAT
A Molecule type: DNA
A Cross references: GB:H9904; NID:g13475
C Genomics: P

```
Query Match      36.0%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	3 AR 4
Db	2 AR 3

Search completed: December 12, 2002, 15:20:09
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 12, 2002, 15:14:30, Search time 6 seconds

Title: US-09-600-432-39

Perfect score: 25

Sequence: 1 PFARI 5

Scoring Table: GAPSW62

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing listed 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	38	0	1	TUFT_HUMAN
2	32	38	0	1	FYFL-ANTEL
3	8	32	0	1	UN05-CIOPA
4	8	32	0	1	UN05-CIOPA
5	7	28	0	1	DMCL-PSECH
6	7	28	0	1	DMCL-PSECH
7	28	0	1	1	RM01-YAST
8	7	28	0	1	RM01-YAST
9	7	28	0	1	ET03-LITRU
10	7	28	0	1	ET03-LITRU
11	7	28	0	1	SI04-ACHRO
12	7	28	0	1	SI04-ACHRO
13	7	28	0	1	SI04-ACHRO
14	7	28	0	1	SI04-ACHRO
15	7	28	0	1	SI04-ACHRO
16	7	28	0	1	SI04-ACHRO
17	7	28	0	1	SI04-ACHRO
18	7	28	0	1	SI04-ACHRO
19	6	24	0	1	SI04-ACHRO
20	6	24	0	1	SI04-ACHRO
21	5	20	0	1	SI04-ACHRO
22	5	20	0	1	SI04-ACHRO
23	5	20	0	1	SI04-ACHRO
24	5	20	0	1	SI04-ACHRO
25	5	20	0	1	SI04-ACHRO
26	5	20	0	1	SI04-ACHRO
27	5	20	0	1	SI04-ACHRO
28	5	20	0	1	SI04-ACHRO
29	5	20	0	1	SI04-ACHRO
30	5	20	0	1	SI04-ACHRO
31	4	16	0	1	SI04-ACHRO
32	4	16	0	1	SI04-ACHRO
33	4	16	0	1	SI04-ACHRO

34	4	16	0	1	SI04-ACHRO
35	4	16	0	1	SI04-ACHRO
36	4	16	0	1	SI04-ACHRO
37	4	16	0	1	SI04-ACHRO
38	4	16	0	1	SI04-ACHRO
39	4	16	0	1	SI04-ACHRO
40	4	16	0	1	SI04-ACHRO
41	4	16	0	1	SI04-ACHRO
42	4	16	0	1	SI04-ACHRO
43	4	16	0	1	SI04-ACHRO
44	4	16	0	1	SI04-ACHRO
45	4	16	0	1	SI04-ACHRO

ALIGNMENTS

RESULT 1	TUFT_HUMAN	STANDARD:	PRT:	4 AA.
ID	TUFT_HUMAN	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DB	Phagocytosis-stimulating peptide (Tutanol)			
OS	Human sapiens (human)			
CC	Eukaryota; Metazoa; Chordata; Cephalochordata; Vertebrata; Euteleostomi;			
OC	Chordata; Vertebrata; Cephalochordata; Cephalochordata; Cephalochordata;			
CC	NCBI:Taxid=9606;			
RN	[1]			
EX	Medline-72187087; PubMed-4112769;			
RA	Nishioka K., Constantopoulos A., Satoh P.S., Meijer V.A.;			
RT	Phagocytosis and synthesis of the phagocytosis			
RL	biochem. Biophys. Res. Commun. 47:172-179(1972).			
RN	[1]			
EX	Medline-6801045; PubMed-416272;			
RA	Tran-Van P., et al.;			
RT	Effect of leucophilic gamma globulin (leucokinin) on the phagocytic			
CC	CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD; LEUCOKININ ON THE			
CC	CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD; LEUCOKININ ON THE			
CC	TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC			
CC	ACTIVITY OF NEUTROPHILS.			
CC	PM: 9147, 92147.			
DN	NCBI:Taxid=9606;			
CC	SEQUENCE 4 AA: 501 MW; 7417632C000000 CDS4;			
50	SEQUENCE 4 AA: 501 MW; 7417632C000000 CDS4;			
Query Match	48.0%; Score 12; DB 1; Length 4;			
Best Local Similarity	100.0%; Pred. No. 1;le=05;			
Matches	2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	1 PR 2			
DD	3 PR 4			
RESULT 2	FYFL-ANTEL	STANDARD:	PRT:	4 AA.
ID	FYFL-ANTEL	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DB	Phagocytosis-stimulating peptide (Tutanol)			
OS	Human sapiens (human)			
CC	Eukaryota; Metazoa; Chordata; Cephalochordata; Vertebrata; Euteleostomi;			
OC	Chordata; Vertebrata; Cephalochordata; Cephalochordata; Cephalochordata;			
CC	NCBI:Taxid=9606;			

RA Wabnitz P.A., Bewis J.N., Taylor M.T., Wallace S.G.
 RT Litor electric. Comparison with the Australian buzzing tree frog
 RT rubella. J. Comp. Zool. 52:639-645(1999).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 KW Amphibian skin; Maturation. AMPHIBION
 SQ SEQUENCE 5 AA: 630 MW: 668761pI2C9A00000 CRC64;
 Query Match Similarity 28.0%; Score 7; DB 1; Length 5;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 P 1
 DB 4 P 4

RESULT 9
 PAPA_PANAMA STANDARD: PRT: 5 AA.
 AC P81864;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pardaxia II (PxiII) (Fragment).
 OS Pardaxius marcosus (Red sea moses sole).
 CC Actinopterygii; Neopterygii; Teleostei; Ruteleostomi;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Pterocetriformes;
 CC Osteichthyes; Osteichthyes; Ruteleostomi; Ruteleostomi;
 OX NCBI_TaxID:31087;
 RN 111998;
 RC TISSUE: Skin secretion;
 RX MEDLINE:87057369; PubMed:1782138;
 RA Lactocytin and lactoferrin are secreted by the skin of the
 RT polypterids from the swimming activity of two deep-sea fishes
 RT marcosus. J. Exp. Zool. 280:1-10(1998).
 CC -1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
 CC PROPERTIES: FORMS VOLTAGE-DEPENDENT, NON-PERMEABLE CHANNELS
 CC -1- SUBMIT: UNKNOWN. IN AQUEOUS SOLUTION EXISTS AS A Tetramer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC TISSUE SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
 FT NOLTER 5 5
 SQ SEQUENCE 5 AA: 614 MW: 776903C9C100000 CRC64;

Query Match Similarity 100.0%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1:le=05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 P 1
 DB 5 P 5

RESULT 10
 PRCI_PFERAM STANDARD: PRT: 5 AA.
 ID PRCI_PFERAM
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 OS Periplaneta americana (American cockroach).
 CC Limulus polyphemus (Atlantic horseshoe crab), and
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Sterygota; Neoptera; Orthoptera; Dictyoptera; Blattaria;
 OC Blattodea; Blattaria; Periplaneta.
 OX NCBI_TaxID:6978, 6850, 6759;
 RN 111998;
 RC SPECIES=P.americana;
 RX MEDLINE:7674798; PubMed:576;
 RT Structure of the pentapeptide proctolin, a proposed neurotransmitter
 RT in insects. J. Insect Physiol. 17:1253-1256(1975).
 CC [6 Sci. 17:1253-1256(1975).]
 RN 3;
 RP BIOLOGICAL SOURCE:
 RC PERILPANE;
 RX MEDLINE:8125865; PubMed:6113690;
 RA O'Shea M., Adams M.E.;
 RT Pentapeptide (proctolin) associated with an identified neuron. J.
 RN Science 117:567-569(1981).
 RP SEQUENCE: Polyphemus;
 RX MEDLINE:8632789; PubMed:2356151;
 RA Groome J.R., Tillinghast E.K., Tomley M.A., Vetrova A.,
 RA Watson W.J., Hunt D.F., Griffin P.K., Alexander J.E..
 RT Identification of proctolin in the central nervous system of the
 RT horseshoe crab, Limulus polyphemus. J. Neurosci. 14:205-211(1994).
 RN 4;
 RP SEQUENCE: Musca;
 RX MEDLINE:8632789; PubMed:2872661;
 RA Stangler J., Dirksen H., Keller R.;
 RT Identification of the proctolin receptor in the central nervous system
 RT of the house crab, Carcinus maenas. J. Neurosci. 7:67-72(1986).
 CC -1- FUNCTION: STIMULATES CHROMATIN AND HISTONE MOTILITY.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 DR PIR: A60411; A60411;
 KW Neuropeptide.
 SQ SEQUENCE 5 AA: 649 MW: 710793M4600000 CRC64;
 Query Match Similarity 100.0%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1:le=05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 P 1
 DB 4 P 4

RESULT 11
 SIQA_ACHDO STANDARD: PRT: 5 AA.
 ID SIQA_ACHDO
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DE Subomphal ganglion pentapeptide.
 OS Acheta domestica (House cricket).
 CC Phrynosoma; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta;
 CC Gryllidae; Gryllinae; Acheta.
 OX NCBI_TaxID:6997;
 RN 111998;
 RC SEQUENCE.
 NA Wicker C., Wicker C.;
 RT Isolation and characterization of a peptide isolated from the
 RT subomphal ganglion of Acheta domestica (orthoptera). J.
 RN Comp. Biochem. Physiol. 88C:185-187(1987).

```

CC -1- SUPERLOCAL LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
DR PTE: JS0319; JS0319.
SQ SEQUENCE 5 AA: 476 MH: 69D760DDDD800000 CRC64:
Query Match 28.0%; Score 7; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 P 1
DB 4 P 4

RESULT 12
ID CIP2_MTTED STANDARD: PRT: 6 AA.
AC 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (blue mussel).
CC Eukaryota; Metazoa; Chordata; Bivalvia; Pluriomorphia; Mytiloidea;
CX Mytiloidea; Mytilidae; Mytilus.
OY NCBI_TaxId=6550;
RN [1]
RW Nucleotide.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=337776; Takahatake I., Ikeda T., Numeoka Y.;
"Structures and actions of Mytilus inhibitory peptides.*";
PL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -1- MUSCLES: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
CC -1- SIMILARITY: TO MIP II.
RW Peptide.
RX MEDLINE=8747696.
RW Nucleotide.
SQ SEQUENCE 6 AA: 637 MH: 720C6875881000 CRC64:
Query Match 28.0%; Score 7; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 P 1
DB 3 P 3

RESULT 13
ID CIP2_MTTED STANDARD: PRT: 6 AA.
AC 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE Contraction-inhibiting peptide II (MIP II).
OS Mytilus edulis (blue mussel).
CC Eukaryota; Metazoa; Chordata; Bivalvia; Pluriomorphia; Mytiloidea;
CX Mytiloidea; Mytilidae; Mytilus.
OY NCBI_TaxId=6550;
RN [1]
RW Nucleotide.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=337776; Takahatake I., Ikeda T., Numeoka Y.;
"Structures and actions of Mytilus inhibitory peptides.*";
PL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -1- MUSCLES: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
CC -1- SIMILARITY: TO MIP I.
RW Peptide.
RX MEDLINE=8747696.
RW Nucleotide.

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```

RW Hormone: Auidation. 6
SQ SEQUENCE 6 AA: 621 MH: 72C5C6876D8B1000 CRC64:
Query Match 28.0%; Score 7; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 P 1
DB 3 P 3

RESULT 14
ID EIO1_LITRU STANDARD: PRT: 6 AA.
AC PE2096-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
OS Eukarya; Rubella (Desert tree frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Amphibia; Anura; Neobatrachia; Bufonidae; Hylidae;
OY NCBI_TaxId=10485;
RN [1]
RW Nucleotide.
RC TISSUE=Skin secretion;
RX MEDLINE=9546455; PubMed=9546455; Tyler M.J., Wallace J.C.;
"Comparison of the amino acid sequences of the skin peptides from Litoria
rubella.*";
PL J. Herpetol. 59:639-645(1995).
CC -1- SUPERLOCAL LOCATION: SECRETED.
RW Amphibian skin; Auidation.
SQ SEQUENCE 6 AA: 792 MH: 6683704772C5A000 CRC64:
Query Match Similarity 28.0%; Score 7; DB 1; Length 6;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 P 1
DB 3 P 3

RESULT 15
ID COW_LEQUE STANDARD: PRT: 6 AA.
AC P428B5;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE Oviductal motility stimulating peptide (Lea-OWM).
CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
CX Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OY Chrysomelidae; Chrysomelinae; Chrysomelidae; Chrysomelidae;
OY NCBI_TaxId=7539;
RN [1]
RW Nucleotide.
RC TISSUE=Read;
RX MEDLINE=1271080; PubMed=205497;
"Structures and actions of Mytilus inhibitory peptides.*";
PL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -1- SIMILARITY: TO MIP I.
RW Peptide.
RX MEDLINE=8747696.
RW Nucleotide.

```

-1- SIMILARITY: TO MIP I. STIMULATES THE CONTRACTIONS OF THE

CG OUTDUCT
KW Neuropeptide: Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 720 MW; 68076245501000 CRC64;
AMIDATION.
Query Match 28.0%; Score 7; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 P 1
Db 5 P 5
Search completed: December 12, 2002, 15:19:18
Job time : 6 secs

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Placentalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1] taxid=1010;

RP SOURCE FROM N.A.

RX MEDLINE=1182758; PubMed=1840486;

RA Sato H., Aono S., Kashiwata S., Koike O.;

RT Genetic defect of Billrubi UDP-glucuronosyltransferase in the

RL Blochmann, Biophys. Res. Commun. 177:1161-1164(1991).

CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

CC EXCRETION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS.

CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR

CC EC: 2.4.1.17; EC: 2.4.1.18; EC: 2.4.1.19; EC: 2.4.1.20;

CC -1- SUBCELLULAR LOCATION: MICROsome.

DR EMBL: S38636; AAB19259.1;

RF Transferase; glycosyltransferase; Microsome; Multigene family.

FT NON-TER 4

FT 4

SQ SOURCE 4 AA; 473 MW; 633732C42000000 CRC64;

Query Match 12.0%; Score 3; DB 11; Length 4;

Best Local Similarity 0.0%; Pred. No. 6.7e05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 5 I 5

Db 2 V 2

RESULT 7

PS1073

ID P83073 PRELIMINARY; PRT: 5 AA.

AC P83073-2001 (Trembel. 18, Created)

DF 01-OCT-2001 (Trembel. 18, Last sequence update)

DT 01-OCT-2001 (Trembel. 18, Last annotation update)

GS Bacillus cereus (Fragment).

OS Bacillus cereus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OC Bacillus cereus; Bacillus.

OC NR017408-139;

RN [1]

RP SOURCE: JMB 11796;

RA Browne N., Dowds B.C.A.;

RL Submitted (JUL-2001) to the SWISS-PROT data bank.

SQ SOURCE 5 AA; 623 MW; 6801AA316F00000 CRC64;

Query Match 8.0%; Score 2; DB 2; Length 5;

Best Local Similarity 0.0%; Pred. No. 1.05e05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 R 2

Db 2 K 2

Search completed: December 12, 2002, 15:18:47

Job time : 22.25 secs

